10/79/101

83z25 clostridium Q97tf6 clostridium

Q8py92 methanogaru Q8py91 methanopyru Q89613 chostridium Q9deg5 gallus gall Q9deh4 gallus gall Q97ka0 chostridium Q97ka0 chostridium Q97ka0 methanopyru Q84km8 streptococc Q8deg7 streptococc Q8deg7 streptococc Q9deg4 gallus gall Q8ny2 canis famil Q8ny22 canis famil Q8ny23 clostridium Q8ny28 clostridium Q8ny28 clostridium Q8ny28 plasmodium

Q8evf1 mycoplasma Q24041 lixiodendro Q25267 leishmania Q81jk9 plasmodium Q8ewu3 mycoplasma Q9phj3 xylella fas Q9gnz4 leishmania Q8cyp1 streptococc Q8cyp1 streptococc

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Loevgren A., Carlson C.R., Eskils K., Kolsto A.B.;
Localization of putative virulence genes on a physical map of the
Bacillus thuringiensis subsp. gelechiae chromosome.";
Curr. Microbiol. 37:245-250(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
EMBL: Y16268; CAA76148.1; --
HSSP; P09598; 1AH7.
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GO; GO:0008270; F:zinc ion binding; IEA.
InterPro; IFR001831; Zn dep PLPC.
FIREMO1831; Zn dep PLPC.
FRINTS; PR00479; FRPHFHLPASEC.
Prodom; P000384; Zn dep_PLPC; 1.
PROSITE; PS00384; Zn dep_PLPC; 1.
SEQUENCE 283 AA; 32387 MW; 4D72E6723F8A68FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
pholipase C.
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01-JUN-1998 (TEMBLRE). 06, Cast sequ
01-JUN-1998 (TEMBLRE). 06, Last sequ
01-OCT-2003 (TEMBLRE). 25, Last anno
Phosphatidyl-degrading phospholipase
Q8GCY3
Q83Z25
Q97TFC
Q8PY92
Q8FY39
Q9DEG5
Q9DEG4
Q97RY6
Q97RY6
Q9DEG4
Q9
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                                                                                                                    STRAIN=Bt13;
PubMed=9732531;
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117.5
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107.5
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052864
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   Q84fif bacillus ce
Q84dk1 listeria se
Q831L2 listeria mo
Q834d4 listeria mo
Q84dk4 listeria mo
Q84dk5 listeria mo
Q84dk5 listeria mo
Q84dk6 listeria mo
Q84dk7 listeria mo
Q84m7 listeria iv
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Q81v27 bacillus an
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                                                                                                  July 27, 2004, 14:37:17; Search time 39 Seconds (without alignments) 2281.439 Million cell updates/sec
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1522
1 MKKKVLALAAMVALAAPVQS......BAQRVTAGYIHLWFDTYVNR
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               GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                                        - protein search, using sw model
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0811V27
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084DK4
084DK3
084DK4
084DK4
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sp_rodent:*
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sp_vertebrate:*
sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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Maximum DB
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Result Š.

283 AA

Score 1257.5; DB 2; Length 283; Pred. No. 3.6e-90;

82.6%; 80.2%;

Best Local Similarity

Query Match

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SKYENFVDIIKNNYIVSDSNGYWNWKGANPEDWIEGAAVAAKQDYPGVVNDTIKDWFVKA 239
                                                                                           121 AKQAKETGAKYFKLAGESYKUKDMKQAFFYLGLSLHYLGDVNQPMHAANFTNLSYPQGFH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Read T.D., Peterson S.N., Tourssee N., Baillie L.W., Paulsen I.T., Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R., Indicated O.A., Helgason E., Rilstone J., Wu M., Kolonay J.F., Beanan M.J., Dodeon R.J., Brinkac L.M., Gwinn M., DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., Benton W.C., Peterson J.D., Popp M., Khouri H.M., Radune D., Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F., Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C., Fraser C.M., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L., Praser C.M., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
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                                                        SKYENPVDTIKNNYIVSDSNGYMNWKGANPEDWIEGAAVAAKQDYPGVVNDTIKDWFVKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLC OR BA0677.
Bacillus anthracis (strain Ames).
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=198094;
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                                                                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phospholipase C.
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GO; GO:0004629; P:phospholipase C activity; IEA.

GO; GO:0008270; F:zinc ion binding; IEA.

InterPro; IPR008947; PLC Nuclease.

InterPro; IPR001531; Zn dep PLPC.

InterPro; IPR001531; Zn dep PLPC.

PRINTS; PR00479; PRPHPHLPASEC.

ProDom; PD003946; Zn dep PLPC; 1.

PROSITE; PS00384; PROKAR_ZN_DEPRN_PLPC; 1.

COMplete proteome.

SEQUENCE 283 AA; 32384 MW; 60C7296E55D468A7 CRC
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MEDLINE=22608414; PubMed=12721629;
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EMBL; AE017026; AAP24690.1; -.
TIGR; BA0677; -.
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MEDLINE=22608415; PubMed=12721630;
NA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Ivanova N., Sorokin A., Anderson I., Galleron N., Lapidus A.,
A kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
A chu L., Mazur M., Golteman E., Larsen N., D'Souza M., Malunas T.,
A drechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
A overbeek R., Kyrpides N.;
A drechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
M. Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis.",
Nature 423:87-91(2003).
Nature 423:87-91(20
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                                                                                                                                                                                                              1 MKKKVLALAAMVALAAPVQSVVFAQTNNSESPAPIL-RWSAEDKHNEGINSHLWIVNRAI
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           32, Indels
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
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283 AA; 32387 MW; 4D72E6723F8A68FF CRC64;
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PROSITE; PS00384; PROKAR_ZN_DEPEND_PLPC; 1.
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              23; Mismatches
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L-JUN-2003 (TrEMBLrel. 24, Last seq
                 227; Conservative
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82.2%; Score 1250.5; DB 2; Length 283;
Best Local Similarity 79.9%; Pred. No. 1.3e-89;
Matches 226; Conservative 24; Mismatches 32; Indels 1;
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"Bacillus cereus pc-plc and sph genes.";

"Bacillus cereus pc-plc and sph genes.";

"Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AY195600; AA040751.1; --

"GO; GO:0004629; F:phospholipase C activity; IEA.

"GO; GO:0008270; F:zinc ion binding; IEA.

"InterPro; IPR001931; Zn dep PLPC.

"Pfam; PF00882; Zn dep PLPC; 1.

"PRINTS; PR00479; PRPHFHLPASEC.

"ProDom; PD003946; Zn dep PLPC; 1.

"PROSITE; PS00384; PROKAR ZN DEPBRD PLPC; 1.

"PROSITE; PS00384; PROKAR ZN DEPBRD PLPC; 1.
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Listeria seeligeri.
Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
NCBI_TaxID=1640;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1396;
240 AVSQEYADKWRAEVTPVTGKRLMEAQRVTAGYIHLWFDTYVNR 282
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                                            241 AVSQEYADKWRAEVIPWTGKRLMDAQRVTAGYIQLWFDTYGDR
                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phosphatidylcholine-specific phospholipase C.
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Q1-JUN-2003 (TrEMBLrel. 24, C. 01-JUN-2003 (TrEMBLrel. 24, L. 01-OCT-2003 (TrEMBLrel. 25, L. Phospholipase (Fragment).
                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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180 SKYENFVDTIKNNYIVS-DSNGYWNWKGANPEDWIEGAAVAAKQDYPGVVNDTIKDWFVK 238
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                                                                 "Mucleic acid-based, cultivation-independent detection of Listeria spin and genotypes of L. monocytogenes.";
FEMS Immunol. Med. Microbiol. 35:215-225(2003).

EMBL; AXISO839; AAO19486.1; -.

GO; GO:0004629; F:phospholipase C activity; IEA.

GO; GO:0004629; F:phospholipase C activity; IEA.

R FROM:FR GO; FREMEPHLARSEC.

R PROM:FR GO; GO:00344; PROKAR ZN DEPEND_PLPC; 1.

R PROSITE; PSO0344; PROKAR ZN DEPEND_PLPC; 1.

R NON TER 275 275

SEQUENCE 275 AA; 31213 MW; 87DA8752CFIBEC18 CRC64;
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FEMS Immunol. Med. Microbiol. 35:215-225(2003).

EMBL; AY150810; AA019477.1; -.

EMBL; AY150840; AA019477.1; -.

GO; GO:0008429; Fiphospholipase C activity; IEA.

GO; GO:0008270; Fizhor ion binding; IEA.

InterPro; IPR001531; Zn dep_PLPC.

Pfam, PF00882; Zn dep_PLPC.

PRINTS; PR00479; PRPHFHLASEC.

PRODOM; PD003946; Zn_dep_PLPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 31.7%; Score 482.5; DB 2; Length 275; Best Local Similarity 36.9%; Pred. No. 16-29; Matches 97; Conservative 54; Mismatches 101; Indels 11;
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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MEDILINE=22535694; PubMed=12648840;
Schmid M., Walcher M., Bubert A., Wagner M., Wagner M.,
Schleifer K.-H.;
Schmid M., Walcher M., Bubert A., Wagner M., Wagner M., Schleifer K.-H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phospholipase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 GLSDSQKDRTWKKAVRAATGKRL 275
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96 PYYDNSTYASHFYDPDTGTTYIPPAKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLH 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.0%; Score 442; DB 2; Length 242; Best Local Similarity 42.6%; Pred. No. 1.36-26; Matches 81; Conservative 38; Mismatches 71; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 242 AA; 27890 MW; 7F3DEFD2AB43B372 CRC64;
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Last sequence update)
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                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
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216 AAVAAKQDYP 225
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                                                        230 NAKRAKRDÝP 239
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SEQUENCE FROM N.A.
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AC 084401
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DT 01-O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 LRWSAEDKHNEGINSHLWIVNRAIDIMSRNTTIVNPNETALLNEWRADLENGIYSADYEN 95
                                                                                                                                                                                                                                                                                                                                               50 SHLWIVNRAIDIMSRNTIIVNPNETALLNEWRADLENGIYSADYENPYYDNSTYASHFYD 109
                                                                                                                                                                                                                                                                                                                                                                               64 THYWLFKQAEKILAKDVNHHRANLANELKKFDKQIAQGIYDADHKNPYYDTSTFLSHFYN 123
                                                                                                                                                                                                                                                                  2 KKKVLALAAMVA-LAAPVQSVV-----PAQT----NNSESPAP-ILRWSAEDKHNEGIN 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 TNLSYPMGFHSKYENFVDTIKNNYIVSDSNGYWNWKGANPEDWIEGAAVAAKQDYP 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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29.0%; Score 442; DB 2; Length 242;
Best Local Similarity 42.6%; Pred. No. 1.3e-26;
Matches 81; Conservative 38; Mismatches 71; Indels
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1 Similarity 39.4%; Score 448; DB 2; Length 242;
93; Conservative 45; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Listeria monocytogenes.
Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
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MEDINE=2253564; Pubmed=12648840;
Schmid M., Walcher M., Bubert A., Wagner M., Schnidid K.-H.;
Schleifer K.-H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27892 MW; 91D9A192EBE4DE18 CRC64;
                                                              242 AA; 27963 MW; CA45226804B99E87 CRC64;
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01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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PROSITE; PS00384; PROKAR_ZN_DEPEND_PLPC; 1.
NON TER 242 242 242
SEQÜENCE 242 AA; 27892 MW; 91D9A192EBE4;
           PROSITE, PS00384; PROKAR ZN DEPEND PLPC; 1.
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SEQUENCE
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Matches
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50 LSWSADNPINTDVNIHYWLFKQAEKILAKDVDHMRANLMNELKNFDKQIAQGIYDADHKN 109
                                                                                                                                PYYDNSTYASHFYDPDTGTTYIPFAKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLH 155
                                                                                                                                                       156 YLGDVNQPMHAANFTNLSYPMGFHSKYENFVDTIKONYIVSDSNGYWNWKGANPEDWIEG 215
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phospholipase (Fragment).
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD003946; Zn_dep_PLPC; 1.
PROSITE; PS00384; PROKAR_ZN_DEPEND_PLPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
    38;
    80; Conservative
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230 NAKRAKRDYP 239
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230 NAKRAKRDHP 239
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SEQUENCE
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Q84DK3;
    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 PYYDTSTFLSHFYNPDKDNTYLPGFANAKITGAKYFNQSVADYREGKFDTAFYKLGLAIH 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 YLGDVNQPMHAANFTNLSYPMGFHSKYENFVDTIKNNYIVSDSNGYWNWKGANPEDWIEG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schleifer K.-H.;

Thus, a schleifer K.-H.;

Thus, and genotypes of L. monocytogenes.";

Rems, and genotypes of L. monocytogenes.";

Rems, and genotypes of L. monocytogenes.";

Rems, and senotypes of L. monocytogenes.";

Rems, proons and senotypes of L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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FEMS. ANTISONS: Microbiol. 35:215-225(2003).

EMBL, ANTISONS: AAO19482.1; -..

GO; GO:0004629; F:phospholipase C activity; IEA.

GO; GO:0004629; F:phospholipase C activity; IEA.

InterPro; IPR00837; P.C. Nuclease.

InterPro; IPR00837; P.C. Nuclease.

InterPro; IPR00837; P.C. Nuclease.

PRINTS; PR00479; FRPHFHLPASEC.

PRODM; PR00479; FRPHFHLPASEC.

PRODM; PR003946; Zn dep_ PLPC; 1.

PROSTER; PS00384; PROKAR_ZN_DEPEND_PLC; 1.
                                                                                                                                                                                                                                                                                                                                                                                             Length 242;
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match 28.9%; Score 440; DB 2; Length 24 Best Local Similarity 42.6%; Pred. No. 1.8e-26; Matches 81; Conservative 37; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBL_TaxID=1639;
MEDLINE=22535694; PubMed=12648840;
Schmid M., Walcher M., Bubert A., Wagner M., Wagner M.,
Schleifer K.-H.;
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Schmid M., Walcher M., Bubert A., Wagner M., Wagner M.,
Schleifer K.-H.;
                                                                                                                                                                                                                                                                                                                           NON_TER 242 242 — — — SEQUENCE 242 AA; 27947 MW; C9BAD440B74F9BC9 CRC64;
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Last sequence update)
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Best Local Similarity
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50 LSWSADNPINIDVNIHYWLFKQAEKILAKDVDHMRANLMNELKNFDKQIAQGIYDADHKN 109
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                                                                                                                                                                                                                                                                                                                        156 YLGDVNQPMHAANFTNLSYPMGFHSKYENFVDTIKNNYIVSDSNGYWNWKGANPEDWIEG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                      36 LRWSAEDKHNEGINSHLWIVNRAIDIMSRNTTIVNPNETALLMEWRADLENGIYSADYEN
                                                                                                                   Gaps
                                                                                                                71; Indels
242 AA; 27865 MW; 7F3DEFD2B1FEDE12 CRC64;
                                                     Match 28.7%; Score 437; DB 2; Local Similarity 42.1%; Pred. No. 3.1e-26; Les 80; Conservative 39; Mismatches 71;
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1.44 1.45

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NON TER
SEQUENCE
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Remail, AY150832; AAO19479.1, -.. GO; GO:0004629; F:phospholipase C activity; IEA.

GO; GO:0008270; F:phospholipase C activity; IEA.

RO; GO:0008270; F:phospholipase.

InterPro; IPR001531; Zn dep_PLPC.

R Pfam; PF00882; Zn dep_PLPC; 1.

R Pfam; PF00893; Zn dep_PLPC; 1.
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MEDLINE-2535694; PubMed=12648840;
MEDLINE-2535694; PubMed=12648840;
Schmid M., Walcher M., Bubert A., Wagner M., Wagner M.,
Schleifer K.-H.;
"Nucleic acid-based, cultivation-independent detection of Listeria app. and genetypes of L. monocytogenes.";
FEMS Immunol. Med. Microbiol. 35:215-225(2003).
EMBL; AY150838; AAO19485.1; -.
GO; GO:0004629; F:phospholipase C activity; IEA.
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27.0%; Score 411; DB 2; Length 236;
Best Local Similarity 42.1%; Pred. No. 3.3e-24;
Matches 80; Conservative 36; Mismatches 68; Indels
                                                                                                                                                                                                                                                                   Listeria monocytogenes.
Bacteria, Firmicutes; Bacillales; Listeriaceae; Listeria.
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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                                                                                                                                     Last sequence update)
Last annotation update)
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                                      PRT;
                            Q84DX6 PRELIMINARY;
Q84DX6,
Q1-JUN-2003 (TYEMBLYEL: 24, C
01-JUN-2003 (TYEMBLYEL: 24, L
01-OCT-2003 (TYEMBLYEL: 25, L
Phospholipase (Fragment).
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AC Q84DK
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50 LSWSADNPTNITDVNITHYWLFKQAEKILAKDVNHMRANLMNELKKFDKQIAQGIYDADHKN 109
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1. STRAIN=NCTC 5105;

2. MEDLINE=22535694; PubMed=12648840;

3. MEDLINE=22535694; PubMed=12648840;

3. MEDLINE=22535694; PubMed=12648840;

4. Schleifer K.-H.;

4. Nucleia caid-based, cultivation-independent detection of Listeria at "Nucleia caid-based, cultivation 35:215-225(2003).

3. FEMS Immunol. Med. Microbiol. 35:215-225(2003).

3. RMLi, ATS0811, AAO19478.1;

3. GO; GO:0008270; F:zinc ion binding; IEA.

3. ROG; GO:0008270; F:zinc ion binding; IEA.

3. RICE-PRO: IPRO01531; Zn. dep_PLPC.

3. REATH: PRO0882; Zn. dep_PLPC.

3. REATH: PRO0882; Zn. dep_PLPC;

3. REATH: PRO08945; Zn. dep_PLPC;

4. REATH: PRO08945; Zn. dep_PLPC;

5. REATH: PRO08945; Zn.
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Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
NCBI_TaxID=1639;
GO; GO:0008270; F:zinc ion binding; IEA.
InterPro; IPR068947; PLC Nuclease.
InterPro; IPR001531; Zn Gep_PLPC.
Ptam; PR00882; Zn Gep_PLPC.
PRINTS; PR00479; PRPHPHLPASEC.
ProDom; PD003946; Zn Gep_PLPC; 1.
PRINT E342 242
SEQÜENCE 242 AA; 27840 MW; C916EE4DAAE7IE8F CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Phospholipase (Pragment).
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Matches 78; Conservative
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110 PDTGTTYIPFAKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANF 169
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SIZIURNE ATCC 19119;

STRAIN=ATCC 19119;

NIGH EV., Goebel W.;

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

L. Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ2498965; CAC80657.1; -.

R. GO: GO:0004629; F:phydrolase activity; IEA.

R. GO: GO:0004629; F:phospholipase C activity; IEA.

R. GO: GO:0008270; F:phospholipase C activity; IEA.

R. GO: GO:0008270; F:phospholipase C activity; IEA.

R. InterPro: IPRO08941; PLC Nuclease.

R. InterPro: IPRO08941; Zn dep PLPC.

R. PRINTS; PRO0479; PRPHPILPASEC.

R. PRINTS; PRO0479; PRPHPILPASEC.

R. Hydrolase.
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=1638;
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SEQÜENCE 154 AA; 17887 MW; FB12EE594D33E39A CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Phospholipase C (EC 3.1.4.3) (Fragment).
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242 SOEYADKWRAEVTPVTGKRLMEAORVTAGYIHLWF 276

182 YENFVDTIKNNYIVSDSNGYWNWKGANPEDWIEGAAVAAKQDYPGVVNDTTKDWFVKAAV 241

Search completed: July 27, 2004, 14:47:21 Job time : 41 Becs Organization of the second of

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: July 27, 2004, 14:32:07; Search time 13 Seconds (without alignments)

1129.522 Million cell updates/sec
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Title: PCT-US03-12556-2
Perfect score: 1522
Sequence: 1 MKKKVLALAAAVQS.......EAQRVTAGYIHLWFDTYVNR 282

Sequence: 1 MKKKVLALAAMVALAAPVQS...
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

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Minimum DB seq length: 0
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Listing first 45 summaries

Database : SwissProt_42:*

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SUMMARIES

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5.8 866 1 5.8 1068 1 5.8 472 1 5.8 484 1 5.8 1656 1 5.7 407 1 5.7 368 1 5.7 857 1		STANDARD;	eat st r (utes;	N.A. 149; PubMed=2536680 Cruz-Rodz A.L., Le	Goebel W.; "A Bacillus cereus cytolytic de comprises the phospholipase C a sequence and genetic linkage."; J. Bacteriol. 171:744-753(1989)	12] SEQUENCE OF 50-142 FROM N.A. Gilmore M.S., Gilmore K.S., Goeb "A new strategy for ordered DNA the rapid purification of near-m	ragment."; ch. 2:108-114(; Required, wit) molysis).	CATALYTIC ACTIVITY: A phosphatidylcholine diacylglycerol + choline phosphate. COFACTOR: Binds 3 zinc ions. SUBUNIT: Monomer.	SIMILARITY: BELONGS TO THE BACTERIAL FAMILY.	OT entry is col Swiss Institute Bioinformatics	non-profit instituand this statement requires a license memail to license	181 181 7. 7; 11; RPH	946; Zn_dep_PLPC;
33.5 33.5 33.6 88.5 88.5 88.5 89.5 44.0 87.5 87.5 87.5 87.5 88.6 88.6 88.6 88.6 88.6 88.6 88.6 88		LT 1 BACCE PHLD BACCE	1994 1994 2003 11ipas phosp	ilus c eria; Taxii	ll) SEQUENCE FROM N.A STRAIN=GP-4; MEDLINE=89123149; Gilmore M.S., Cru	Goebel W.; "A Bacillus comprises the sequence and J. Bacteriol.	SEQUENCE OF 5 Gilmore M.S., "A new strate the rapid pur	restriction fragment."; Gene Anal. Tech. 2:108	-!- CATALYTIC ACTIVITY diacylglycerol + -!- COFACTOR: Binds :-!- SUBUNIT: Monomer	-!- SIMILARIT FAMILY.	This SWISS-PR between the the European	use by non- modified and entities requ or send an em	EMBL, M34149; AAA9 EMBL, M35411; AAA2 PIR, S18978; PS019 HSSP, P09598; IAH7 InterPro; IPR00894 InterPro; IPR00153 Pfam; PF00882; Zn PRINTS; PR00479; P	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 AKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANFTNLSYPMGFH
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MEDLINE=93249510; PubMed=8387306;
Kuzmin N.P., Gavrilenko I.V., Krukov V.M., Karpov A.V.;
Kuzmin B.P., Gavrilenko I.V., Krukov V.M., Karpov A.V.;
Kuzmin B.C., Gavrilenko of phospholipase C and sphingomyelinase genes
from Bacillus cereus BKM-B164 (letter).";
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<u>PUS5584...</u>
01-MAR-1989 (Rel. 10, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Phospholipase C precursor (EC 3.1.4.3) (PLC) (Phosphatidylcholine cholinephosphohydrolase) (Cereolysin A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

82.4%; Score 1253.5; DB 1; Length 283;
Best Local Similarity 79.9%; Pred. No. 3.7e-92;
Matches 226; Conservative 23; Mismatches 33; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 AVSQEYADKWRAEVTPVTGKRIMBAQRVTAGYIHLWFDTYVNR 282
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MEDLINE=88313678; PubMed=3137122;
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283 AA;
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MEDLINE=88296483; PubMed=2841128; Yamada A., Tsukagoshi N., Udaka S., Sasaki T., Makino S., Nakamura S., Little C., Tomita M., Ikezawa H.; Little Ct., Tomita M., Ikezawa H.; "Nucleotide sequence and expression in Escherichia coli of the gene coding for sphingonyelinase of Bacillus cereus."; Eur. J. Blochem. 175:213-220(1988).
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MEDLINE-89159438; PubMed=2493587;
MEDLINE-89159438; FubMed=2493587;
MUNGH R., Hansen L.K., Birknes B., Jynge K., Hansen S., Hordvik A.,
Little C., Dodson E., Derewend Z.,
"High-resolution (1.5 A) crystal structure of phospholipase C from
                                                                                                                                       SEQUENCE OF 39-65.
MEDLINE=78043154; PubMed=72664;
Otnaess A.-B., Little C., Sletten K., Wallin R., Johnsen S.,
Flengsrud R., Prydz H.;
Flengsrud R., Prydz H.;
Rome characteristics of phospholipase C from Bacillus cereus.";
Eur. J. Biochem. 79:459-468(1977).
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InterPro; IPR008947; PLC Nuclease.
InterPro; IPR008947; PLC Nuclease.
InterPro; IPR00894; Zn dep PLPC.
Pfan; PR008479; PRPHPHLPASEC.
ProDom; PR00479; PRPHPHLPASEC.
ProDom; PR003946; Zn dep PLPC; 1.
Hydrolase; Zinc; Signal; Zymogen; Hemolysis; 3D-structure.
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EMBL; X12854; CAA31332.1; -.
EMBL; X12711; CAA31213.1; -.
EMBL; X54140; CAA45501.1; ALT_TERM.
PIR; $18978; PS0197.
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POTENTIAL
                                                                              SEQUENCE FROM N.A.
STRAIN-EGD-e / Serovar 1/2a;
MEDLINE-21537279; Pubmed=11679669;
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STRAIN=EGD /
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  AKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANFTNLSYPMGFH 179
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                                                                                                                                                                                                                       1 MKKKVLALAAMVALAAPVQSVVFAQTNNSESPAPIL-RWSAEDKHNEGINSHLWIVNRAI
                                                                                                                                                                                                                                            DIMSRNTTIVNPNETALLNEWRADLENGIYSADYENPYYDNSTYASHFYDPDTGTTYIPF
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                                                                                                                                                                                                   Gaps
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1903 (Rel. 14, Last annotation update)
Phospholipase C precursor (EC 3.1.4.3) (PLC) (Phosphatidylcholine cholinephospholydrolase) (Lecithinase).
PLCS OR PRTC OR LMO0205.
Listeria monocycosnes.
Bacteria, Pirmicutes; Bacillales, Listeriaceae; Listeria.
NCBL_TaxID=1639;
                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vazquez-Boland U.-A., Kocks C., Dramsi S., Ohayon H., Geoffroy Mengaud J., Cossart P.; "Nucleotide sequence of the lecithinase operon of Listeria monocytogenes and possible role of lecithinase in cell-to-cell spread.";
                                                                                                                                                                                   DB 1; Length 283;
                                                                                                                                                                                  Query Match 82.3%; Score 1252.5; DB 1; Length Best Local Similarity 80.2%; Pred. No. 4.4e-92; Matches 227; Conservative 23; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                   240 AVSQEYADKWRAEVTPVTGKRLMEAQRVTAGYIHLWFDTYVNR 282
                                                                                                                                                                                                                                                                                                                                           32383 MW; AC5452EFF2E22B19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      289 AA
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283 AA;
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P33378;
01-FEB-1994 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glaser P., Frangeul L., Buchteser C., Rusnick C., Amend A.,
Glaser P., Frangeul L., Buchteser C., Rusnick C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
A Charbit A., Chectouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Bntian K.-D., Faihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L. M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A Madueno E., Matcournam A., Mata Vicente J., Noy E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A Warquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91267617; PubMed=1904842; Geoffroy C., Raveneau J., Beretti J.L., Lecroisey A., Vazquez-Boland J.-A., Alouf J.E., Berche P.; Vazquez-Boland J.-A., Alouf J.E., Berche P.; Purification and characterization of an extracellular 29-kilodalton phospholipase C from Listeria monocytogenes."; Infect. Immun. 59:2382-2388 [1991].
-! FUNCTION: IMPORTANT ROLE IN THE INFECTIOUS PROCESS. MAY CONTRIBUTE TO BEFICIENT LYSIS OF THE TWO-MEMBRANE VACUOLES THAT SURROUND THE BACTERIA AFTER DIRECT CELL-TO-CELL SPREAD.
-! CATALYTIC ACTIVITY: A phosphatidylcholine + H(2) O = 1,2-diacylglycerol + choline phosphate.
-!- COFACTOR: Binds 3 zinc ions (By similarity).
-!- SIMILARITY: BELONGS TO THE BACTERIAL ZINC-METALLOPHOSPHOLIPASES C
STRAIN=EGD / Serovar 1/2a;
MEDLINE=22258410; PubMed=1582425;
Domann E., Wehland J., Rohde M., Pistor S., Hartl M., Goebel W.,
Domann E., Wehland J., Rohde M., Whensher M., Chakraborty T.;
"A novel bacterial virulence gene in Listeria monocytogenes required
for host cell microfilament interaction with homology to the
proline-rich region of vinculin.";
EMBO J. 11:1981-1990(1992).
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EMBL; X59723; CAA42408.1; -
EMBL; AL591974; CAA0732.1; -.
PIR; AZ100, AF1100,
PIR; S20889; S20888.
HSSP; P09598, 1AH7.
Listilist; LM000205; -.
LinterPro; IPR008947; PLC Nuclease.
InterPro; IPR008947; PLC Nuclease.
InterPro; IPR00837; Zn dep_PLPC.
Pfam; PF00882; Zn dep_PLPC.
Pfam; PR00479; PRPHPHLPASEC.
ProDom; P0003946; Zn dep_PLPC; 1.
PROSITE; PS00384; PROKAR_ZN DEPEND PLPC; 1.
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                    REVIEW
 SHLWIVNRAIDIMSRNTTIVNPNETALLNEWRADLENGIYSADYENPYYDNSTYASHFYD 109
                                                                                                                                                                                                   64 THYWLFKQAEKILAKDVNHMRANLMNELKKFDKQIAQGIYDADHKNPYYDTSTFLSHFYN 123
                                                                                                                                                                                                                                   PDTGTTYIPFAKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANF 169
                                                                                                                                                                                                                                                                           TNLSYPMGFHSKYENFVDTIKNNYIVSDSNGYWNWKGANPEDWIEGAAVAAKQDYPGVVW 229
                                                                                                                                                                                                                                                                                               243
                                                                                                                                                                   63
                                                                                                                                                           2 KKKVLALAAMVA-LAAPVQSVV-----PAQT----NNSESPAP-ILRWSAEDKHNEGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Teo J.Y., Siebel C., "Cloning and expression of the phospholipase C gene from Clostridium perfringens and Clostridium bifermentans.";
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ATCC 638; Macde=10377104; MEDINE=9997183; PubMed=10377104; MEDINE=9997183; PubMed=10377104; Miller L., Bolgiano B., Crane D.T., Miller J., Holley J., Jayasekera P., Titball R.W.; "Differences in the carboxy-remainal [putative phospholipid binding) "Differences in the carboxy-remainal [putative phospholipid binding) domains of Clostridium perfringens and Clostridium bifermentans phospholipases C influence the hemolytic and lethal properties of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=KZ 1012;
Karasawa T., Wang X., Maegawa T., Michiwa Y., Miwa K., Nakamura S.;
"C. sordellii phospholipase C.";
                                                                                                                                                                                                                                                                                                                                                                                           PHLC_CLOBI STANDARD; PRT; 398 AA.

904019, 9804024, 098532;
01-FBB-1991 (Rel. 17, Last sequence update)
01-FBB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Phospholipase C precurence (EC 3.1.4.3) (PLC) (Phosphatidylcholine cholinephosphohydrolase) (Cbp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium bifermentans.
Bacteria, Firmicutes; Clostridia, Clostridiales; Clostridiaceae;
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                                                                                                                                                                                                                                                                                                                                244 AKTKKSYLVG-----NSEWKKDTVEPTGARLRDSQQTLAGFLEFW 283
                                                                                                        Length 289;
          (BY SIMILARITY)
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ZINC 1 (BY SIMILARITY).
ZINC 1 AND 3 (BY SIMILARITY
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
K -> N (IN REF. 2).
I -> T (IN REF. 2).
D -> G (IN REF. 2).
W, 0F35A2A3EDA6E372 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND CONSTRUCTION OF A HYBRID ENZYME.
                                                                                                       33.6%; Score 511; DB 1; 37.1%; Pred. No. 2.2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ATCC 638;
MEDLINE=89108588; PubMed=2536356;
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                                                                                   33277 MW;
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PREVIEW.

**REDLINE-20465460; PubMed=11008117;

**REDLINE-20465460; PubMed=11008117;

**Tegron M., Titball R.W.;

**Tegron M., Tegron M., Te
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SIMILARITY: BELONGS TO THE BACTERIAL ZINC-METALLOPHOSPHOLIPASES C
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(VIA CARBONYL OXYGEN)
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InterPro; IPR001024; Lipoxygenase_LH2.
InterPro; IPR001031; PLAT_LH2.
InterPro; IPR001031; Zn_dep_LPC.
Pfam; PR00131; Zn_dep_LPC; 1.
Pfam; PR00147; PLAT; 1.
Pfam; PR001403; ERPHFHI.PASC.
ProDom; PD003946; Zn_dep_PLPC; 1.
PR051TE; PS50095; PLAT; 1.
PR051TE; PS50095; PLAT; 1.
Hydrolase; Toxin; Hemolysis; Calcium; Calcium-binding; Zinc;
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                    SCVYKEAMENPSFNKWMTQNSIKYAKIA------KDLYYSHSTMSHSWDDW-- 243
                                                                                                                                                                                                                  40 AEDKHNEGINSHLWIVNRAIDIMSRNTTIVNPNET-----ALLNEWRADLENGIYSAD 92
                                                                                                                                                                                                                                       26 AWDGKKDGTGTHSLIAEHGLSMLNND---LSGNESQQVKDNIKILNEYLGDLKLGSTYPD 82
                                                                                                                                                                                                                                                                                                          QQAPPYLGLSLHYLGDVNQPMHAANFTNLSYPMGFHSKYENFVDTIKNNYIVSDS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jepson M., Titball R.W.;

"Structure and function of clostridial phospholipases C.";

"Structure and function of clostridial phospholipases C.";

Microbes Infect. 2:1277-1284(2000).

-!- FUNCTION: Bacterial hemolysins are exotoxins that attack blood cell membranes and cause cell rupture. Binds to eukaryotic membranes where it hydrolyzes phosphatidylcholine, sphingomyelin and phosphatidylethanolamine. The diacylglycerol produced can activate both the arachidonic acid pathway, leading to modulation of the inflammatory response cascade and thrombosis, and protein kinase C, leading to activation of eukaryotic phospholipases and
                                                                                                                                                                                             54; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Phospholipase C precureor (EC 3.1.4.3) (PLC) (Phosphatidylcholine
cholinephosphohydrolase).
                       (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clostridium sordellii.
Bacteria; Pirmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Karasawa T., Wang X., Maegawa T., Michiwa Y., Miwa K., Nakamura "C. sordellii phospholipase C.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
CALCIUM 2 (BY SIMILARITY).
CALCIUM 2 (BY SIMILARITY).
CALCIUM 2 (VIA CARBONYL OXYGEN)
SIMILARITY).
                                                                                          2 AND 3)
                                                                                                                                                                       Length 398;
                                                                                                                                                                                             95; Indels
                                          CALCIUM 3 (BY SIMILARITY).
CALCIUM 2 (BY SIMILARITY).
CALCIUM 1 (BY SIMILARITY).
CALCIUM 1 (BY SIMILARITY).
SRNS -> ARTQ (IN REF. 2 AND
GNT -> ENI (IN REF. 3).
                                                                                                                                               0B628AFE7146BC56 CRC64;
                                                                                                                                                                     16.7%; Score 254; DB 1; 26.9%; Pred. No. 7.1e-13;
                                                                                                           L -> S (IN REF. 3)
G -> D (IN REF. 3)
R -> K (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                                   252 EVTPVTGKRLMEAQRV-TAGYIHLWFDTYVN 281
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                                                                                                                                                 45366 MW;
                                                                                                                                                                     Query Match
Best Local Similarity 26.93
Matches 73; Conservative
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398 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PHOSPHOLIPASE C.
PHOSPHOLIPASE C.
LINKER.
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further membrane damage (By similarity)
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                                       YENPYYDNSTYASHFYDPDTGTTYI------PFAKHAKETGAKYFNLAGQAYQNQDM 143
                                                                                                                                                                                                      204 WKGANPEDWIEGAAVAAKQDYPGVVNDTTKDWFVKAAVSQEYADKWRAEVTPVTGKRLME 263
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-I-CATALYTIC ACTIVITY: A phosphatidylcholine + H(2)0 = 1,2-
diacylglycerol + choline phosphate.

-I-COPACTOR: Blinds 3 zinc and 3 calcium ions.

-I-COPACTOR: Blinds 3 zinc and 3 calcium ions.

-I-DOMAIN: The protein is composed of 2 domains; the N-terminal domain contains the phospholipase c active site (PLC), in a cleft which is also occupied by the 3 zinc ions. The C-terminal domain is a putative phospholipid-recognition domain, which shows structural homology with phospholipid-binding 2-like domains from a range of eukaryotic proteins. The ability to bind membrane phospholipids in a Ca(2+) dependent manner and toxicity is
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Jepson M., Titball R.W.;
Jepson M., Titball R.W.;
Jepson M., Titball R.W.;
Jepson M., Titball R.W.;
Microbes Infect. 2:1277-1284(2000).

-i- FUNCTION: Bacterial hemolysins are exotoxins that attack blood cell membranes and cause cell rupture. Constitutes an essential virulence factor in gas gangrene. Binds to eukaryotic membranes where it hydrolyzes both phosphatidylcholine and sphingomyelin, causing cell rupture. The diacylglycerol produced can activate both the arachidonic acid pathway. Leading to modulation of the inflammatory response cascade and thrombosis, and protein kinase inflammatory response cascade and thrombosis, and protein kinase C, leading to activation of eukaryotic phospholipases and further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=SWCP,
MEDINE=22005774; PubMed=12009886;
MEDINE=220057774; PubMed=12009886;
MEDINE=220057774; PubMed=12009886;
Jost H., Walker N., Bullifent H.L., Songer G., Bueschel D.M.,
Jost H., Wallor C.E., Miller T., Moss D.S., Titball R.W., Basak A.K.;
"The first strain of Clostridium perfringens isolated from an avian
source has an alpha-toxin with divergent structural and kinetic
properties.";
Biochemistry 41:6253-6262(2002).
                                                                                                                                  QQAFFYLGLSLHYLGDVNQPMHAANFTNLSYPMGFHSKYENFVDTIKNNYIVSDSNGYWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2004 (Rel. 43, Last sequence update)
Phospholipase C precursor (EC 3.1.4.3) (PLC) (Phosphatidylcholine cholinephosphohydrolase) (Alpha-toxin) (Hemolysin) (Lecithinase).
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Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Titball R.W., Naylor C.E., Basak A.K.; "The Clostridium perfringens alpha-toxin."; Anaerobe 5:51-64(1999).
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ANGSTROMS) OF THE OPEN FORM.
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conferred by this C-terminal domain, which also contributes to the
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                     sphingomyelinase activity.
MISCELLANBOUS: This bacteria was isolated from a diseased swan.
SIMILARITY: Contains 1 PLAT domain.
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InterPro; IPR008976; PLAT_LH2.
InterPro; IPR008977; PLC Nuclease.
InterPro; IPR0018917; DLG Nuclease.
InterPro; IPR0018917; DLG GPP_PPC.
Pram; PR00882; Zn dep_PLPC; 1.
PRINTS; PR00479; PRPHPHLPASEC.
PRODOM; PD003946; Zn dep_PLPC; 1.
PROSTIE; PS500394; PLAT; I.
PROSTIE; PS00389; PLAT; I.
Hydrolase; Toxin; Hemolysis; Calcium; Calcium-binding; Zinc;
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ZINC 1.
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PHOSPHOLIPASE C.
PHOSPHOLIPASE C.
LINKER.
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les 79; Conservative
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273 214 -NSWSKEFPARSFAKTAKDLYYSHANMSCSWDEWDYAARVA-----LANSQKGTSGYIY 265 Katayama S.-I., Matsushita O., Minami J., Mizobuchi S., Okabe A.; "Comparison of the alpha-toxin genes of Clostridium perfringens type A and C strains: evidence for extragenic regulation of transcription."; Infect. Immun. 61:457-463(1993). SEQUENCE FROM N.A.
STRAIN=NCTC 8237 / ATCC 13124 / CN 1491 / Type A;
STRAIN=NCTC 8237 / ATCC 13124 / CN 1491 / Type A;
MEDLINES=89313290; PubMed=2546005;
Lealie D., Fairweather N., Pickard D., Dougan G., Kehoe M.;
"Phospholipase C and haemolytic activities of Clostridium perfringens alpha-toxin cloned in Escherichia coli: sequence and homology with a 228 VNDTTKDW---FVKAAVSQEYA-----DKW--RAEVTPVTGKRLMEAQRVTAGYIH the phospholipase C gene from Clostridium P15310; P94658; 046246; 046279; 046280; 046281; 046282; 057317; 059303; 059304; 059305; 059313; 060121; 01.2PR-1990 (Rel. 14, Created) 28-FBS-2003 (Rel. 41, Last sequence update) 10.0CT-2003 (Rel. 42, Last annotation update) Phospholipase C precursor (EC 3.1.4.3) (PLC) (Phosphatidylcholine cholinephosphohydrolase) (Alpha-toxin) (Hemolysin) (Lecithinase). PLC OR CPA OR CPE0036. SEQUENCE FROM N.A., AND SEQUENCE OF 29-39.
STRAIN=NCTC 8237 / ATCC 13124 / CN 1491 / Type A;
MEDLINE=89228034, PubMed=2540749;
Okabe A., Shimizu T., Hayashi H.;
"Cloning and sequencing of a phospholipase C gene of Clostridium Clostridium perfringens. Bacteria; Pirmicutes; Clostridia; Clostridiales; Clostridiaceae; STRAIN=8-6 / Type A;
MEDLINE=90188507; PubMed=2560137;
Saint-Joanis B., Garnler T., Cole S.T.;
"Gene cloning shows the alpha-toxin of Clostridium perfringens contain both sphingomyelinase and lecithinase activities.";
Mol. Gen. Genet. 219:453-460(1989). SEQUENCE FROM N.A., AND SEQUENCE OF 29-53.
STRAIN=NCTC 8237 / ATCC 13124 / CN 1491 / Type A;
MEDLINE=89108574; Pubmed=2536355;
Titball R.W., Hunter S.E.C., Martin K.L., Morris B.C.,
Shuttleworth A.D., Rubidge T., Anderson D.W., Kelly D.C.;
"Molecular cloning and nucleotide sequence of the alpha-toxin (phospholipase C) of Clostridium perfringens.";
Infect. Immun. 57:367-376(1989). SEQUENCE FROM N.A., AND CHARACTERIZATION. STRAIN=NCTC 8237 / ATCC 13124 / CN 1491 / Type A; MEDLINE-89108588; PubMed=2536355; Biochem. Biophys. Res. Commun. 160:33-39(1989) 398 AA bifermentans."; SEQUENCE FROM N.A., AND CHARACTERIZATION PRT; Bacillus cereus phospholipase C."; Mol. Microbiol. 3:383-392(1989). SEQUENCE FROM N.A. STRAIN=NCIB 10662 / Type C; MEDLINE=93138764; Pubmed=8423073; "Cloning and expression of the pr perfringens and Clostridium bifer Infect. Immun. 57:468-476(1989). STANDARD; ., Siebel C.; NCBI_TaxID=1502; perfringens CLOPE TSO J.Y CLOPE ઠ 셤

SEQUENCE FROM N.A.

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[13]
MUTAGENESIS OF THR-300, AND CONSERVED ASPARTATE AND TYROSINE RESIDUES.
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STRAIN-NTC 8237 / ATCC 13124 / CN 1491 / Type A;
MEDLINE=20389543; PubMed=10931204;
Alape-Giron A., Flores-Diaz M., Guillouard I., Naylor C.E.,
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MEDLINE=95173092; PubMed=7868589;
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MEDLINE=21664373; PubMed=11792842;
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CER 89L1216 / Type A;
MEDLINE=96146062; PubMed=8581165;
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STRAIN-NCTC 8237 / ATCC 13124 / CN 1491 / Type A;
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Local Similarity 27.1%; Score 229; DB 1; Length 398;
Local Similarity 27.1%; Pred. No. 6.8e-11;
Les 82; Conservative 44; Mismatches 109; Indels 68; Gaps
                                                                       Alape-Giron A.,
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involvement of arachidonic acid metabolism.";
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QGVSILENDLSKNEPESVRKNLEILKENMHELQLGSTYPDYDKNAYD--LYQDHFWDPDT 102
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28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last ennotation update)
Phospholipase C precursor (EC 3.1.4.3) (FLC) (Phosphatidylcholine cholinephosphohydrolase) (Beta toxin).
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Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sphingomyelinase activity.
SIMILARITY: BELONGS TO THE BACTERIAL ZINC-METALLOPHOSPHOLIPASES C
                                                                                                                                                                                                                                                                                                                                                          STRAIN=CL49 / Type A;
MEDLINE=96099301; PubMed=8522524;
Tsutsui K., Minami J., Matsushita O., Katayama S.-I., Taniguchi Y.,
Nakamura S., Nishioka M., Okabe A.;
"Phylogenetic analysis of phospholipase C genes from Clostridium
perfaringens types A to E and Clostridium novyi.";
J. Bacteriol. 177:7164-7170(1995).
                                                               28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Phospholipase C precursor (EC 3.1.4.3) (PLC) (Phosphatidylcholine cholinephosphohydrolase) (Gamma-toxin)
                                                                                                                                                                                                        Clostridium novyi.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taguchi R., Ikezawa H.;
"Phospholipase C from Clostridium novyi type A. I.";
Biochim. Biophys. Acta 409:75-85(1975).
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Interpro; IPR008976; PLAT LH2.
Interpro; IPR008947; PLC Nuclease.
Interpro; IPR001531; Zn_dep_PLPC.
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MEDLINE=20465460, PubMed=11008117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=IID 140 / Type A;
MEDLINE=76040159; Pubmed=241423;
                                                    (Rel. 41, Created)
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                                                                                                                                                                                                                                                               Clostridium.
                                                 28-FEB-2003
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
01-0CT-1996 (Rel. 34, Last annotation update)
01-0CT-1996 (Rel. 34, Last annotation update)
01-0CT-1996 (Rel. 34, Last annotation update)
03-0CT-1996 (Rel. 34, Last annotation u
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Pfam; PF01477; PLAT; 1.
Pfam; PF00882; Zn dep_PLPC; 1.
PRINTS; PR00479; PRPHPHLPASEC.
ProDom; PD003946; Zn dep_PLPC; 1.
PROSITE; PS50095; PLAT; 1.
PROSITE; PS00384; PROKAR ZN_DEPEND_PLPC; 1.
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CALCIUM 2 (WIA CARBONYL OXY SIMILARITY).
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                                                                                                                                    BY SIMILARITY.
PHOSPHOLIPASE C.
PHOSPHOLIPASE C.
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Best Local Similarity 25.5<sup>5</sup>
Matches 66; Conservative
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398 AA;
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P52911;
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                                                                                                                                                                                                                                                      Murphy L., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Successive hydrolysis of beta-D-glucose units from the non-reducing ends of 1,3-beta-D-glucans, releasing alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential).
-!- SIMILARITY: Belongs to cellulase family A (family 5 of glycosyl
hydrolases).
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GO; GO:0004378; F:glucan 1,3-beta-glucosidase activity; IDA.
InterPro; IPR001547; Glyco hydro_5.
Pfam, PF00150; cellulase; I.
PROSITE; PS00659; GLYCOSYL HYDROL F5; 1.
Cell wall; Hydrolase; Glycosidase; Glycoprotein; Signal;
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N-LINKED (GLCNAC. . .) (POTE
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63508 MW; 5814509CC3D93F73 CRC64;
                                                                                                                               Correa J., Vazquez de Aldana C., San Segundo P., del Re;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
Saccharomycetales; Saccharomycetaceae; Saccharomyces
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EMBL; Z70202; CAA94100.1; -.
EMBL; Z68229; CAA92719.1; -.
PIR; S55516; 555516.
HSSP; P07985; 1CEO.
GermOnline; 140753; -.
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                                NCBI_TaxID=4932;
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or send an email to license@isb-sib.ch)
                                                                   PIR; T39569; T39569.
PIR; T43432; T43432.
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SEQUENCE FROM N.A.
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Q56113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
------HYFNLTGANYSSQDI-----LVDHH------HYEVFTD 340
                                172 LSYPMGFHSKYENFV---DTIKNNY----IVSDSNGYWNWKGANPE--DWIEGAAVAAK 221
                                                          341 AQLAETQFARIENIINYGDSIHKELSFHPAVVGE------WSGAITDCATWLNGVGVGAR 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Katayama S., Dai H., Arellano M., Perez P., Toda T., "Fission yeast alpha-glucan synthase Mokl localizes closely with actin and play a role essential for cell morphogenesis and protein kinase C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: UDP-glucose + {alpha-D-glucosyl-(1,3)}(N) UDP + {alpha-D-glucosyl-(1,3)}(N+1).
                                                                                                                        395 YDGSYYNTTLFTINDKPVGTCISQNSLADWTQDYRDRV-RQFIEAQLAT 442
                                                                                                    222 QD--YPGVVNDTTKDWFVKAAVSQEYADKWRAEVTPVTGKRLMEAQRVT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the glycosyltransferase family 1.
                                                                                                                                                                                                                       MOKD_SCHPO STANDARD; PRT; 2358 AA.
094713; 094638;
16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cell wall alpha-1,3-glucan synthase moki3 (EC 2.4.1.183).
MOK13 OR SPRG16D10,05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1,3) } (N+1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces
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56 NRAIDIMSRNTTIVNPNETALLNEWRADLENGIYSADYENPYYDNSTYASHFYDPDTGTT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 YIPFAKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLHYLGD---VNQPMHAANFTNL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 -----ETG---FRNGGDIIGLKÖSLDYLEIMGIKVIYIAGTPFLNQPWGADQYSPL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 DYTILDHHSGTIAQWRDTIEEIHRRGFYLVLDLTISTLGDLIGFRKYLNSTTPFSLFEHE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---KDNYIVSDSNGYWNW-----KGANPEDWIE-GAAVAAKQDYPGVVND----- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 AVWKSNVIYPD----WNFTNKYDPKCBLPRFWGEDGAPVVI---DYVGCYDSDFDQYGDTE 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---TTKDW---FVKAAVSQEYADKWRAEVT--------PVTGKRLMEAQRVTAG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 AFGTHDDWERQLSKFASVQDRLKEWRPSVSEKLKHFACMIIAMLDVDGFRIDKATQITVD 315
                                                                                                                                                                                                                                                                                                                                                                                         3 KKVLALAAMVALAAPVQSVVFAQ-----TINNSESPAPILRWSAEDKHNEGINSHLWIV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Wungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooke K., Chillingworth T., Connerton P., Cronin A., Davies R.M., Dowd L., White N., Farrar J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNILVLNLILSIPRLVFTAKYDERESLWNLNQNQSATDPLDYWGKWENHQYHPSPDDWQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------PFYTVILDKWK-----DGDPRNNEANNTIYEYDIY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Outer membrane protein F precursor (Porin ompF) (Outer membrane
DB 1; Length 2358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fernandez-Mora M., Calva E.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 SYPM-----GFHSKYBNFVDTI----
                                                                                                                                                                                                                                             6.7%; Score 102; DB 1; L
18.4%; Pred. No. 6.9;
Ive 43; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 AA
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OMPF OR OMPS3 OR STY1002 OR T1935.
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                                                                                                                                                                                                                                                                                    18.4%;
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                                                                                         SUBUNIT: Homotrimer (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
SIMILARITY: Belongs to the Gram-negative porin family.
Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR003229; OMP 2.
Interpro; IPR003229; OMP 2.
Interpro; IPR001702; Porin Gram-ve.
Pfam; PF00267; Gram-ve porins; 1.
PRINTS; PR00182; ECOLNEIPORIN.
PROBITS; PD000809; OMP 2; 1.
PROBITS; PS00576; GRAM NEG PORIN; 1.
Otter membrane; Transmembrane; Porin; Phage recognition; Signal;
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PERIPLASMIC (BY SIMILARITY).
BY SIMILARITY.
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PERIPLASMIC (BY SIMILARITY).
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EXTRACELLULAR (BY SIMILARITY).
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EXTRACELLULAR (BY SIMILARITY).
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PERIPLASMIC (BY SIMILARITY).
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EXTRACELLULAR (BY SIMILARITY).
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EXTRACELLULAR (BY SIMILARITY)
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EXTRACELLULAR (BY SIMILARITY)
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PERIPLASMIC (BY SIMILARITY).
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PERIPLASMIC (BY SIMILARITY).
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BY SIMILARITY.
PERIPLASMIC (BY SIMILARITY)
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EMBL; AL627268; CAD05399.1; -.
EMBL; AE016840; AA069550.1; -.
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143
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                                                                                                                                                                                                                                                                                                                                                                                                                144 QOAFFYL--GLS--LHYLGDVNQPMHAANFTN---LSYPM-----GFHSKYENFVDTI 189
                                                                                                                                                                                                                                                                                                                 53 NADQTYAQIGFKGETQINTDLTG-FGQWEYRTKADRAEGEQQNSNLVRLAFAGLKYAEVG 111
                                                                                                                                                                                                                  55
                                                                                                                                                                                                                                   2 MKRKILAAVIPALLAAATANA--AEIYNKDG------NKLDLYGKAVGRHVWTTTGDSK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SERALIBLET2 / SGSC1412 / ATCC 700720;
MEDLINE_21534948 bubMed=11677609;
MEDLINE=21534948 bubMed=11677609;
MCDLINE=21534948 bubMed=11677609;
MCDLINE=21534948 bubMed=11677609;
COUTTNEY L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Mayuyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 413:852-856 (2001).
-!- FUNCTION: OMPF IS A PORIN THAT FORMS PASSIVE DIFFUSION PORES WHICH
-!- FUNCTION: OMPF IS A PORIN THAT FORMSPHILIC MATERIALS ACROSS THE
ALLOW MALL MOLECULAR WEIGHT HYDROPHILIC MATERIALS ACROSS THE
OUTER MEMBERANE. IT IS ALSO RECEPTOR FOR THE BACTERIOPHAGE T2 (By
                                                                                                                                                                                                                                                                                                                                                  SADYENPY - - - YDNSTY - - - ASHFYDPDTGTTY I PFAKHAKETGAKY FNLAGQAYQNQDM
                                                                                                                                                                                                                                                                                                                                                                        164 ---FFGLVDGLSFGIQYQGK-NQDNHSINSQNGDGVGYTMAYEFDGFGVTAAYSNSKRT-
                                                                                                                                                                                                                1 MKKKVLALAAMVALAAPVQSVVFAQTNNSESPAPILRWSAEDKHNEGINSHLWIV----
                                                                                                                                                                                 81; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Homotrimer (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Outer membrane protein F precursor (Porin ompF) (Outer membrane protein IA) (Outer membrane protein IA) (Outer membrane protein IA)
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Enterobacteriaceae, Salmonella.
                                                                                                                                                 DB 1; Length 363;
               BY SIMILARITY.
PERIPLASMIC (BY SIMILARITY).
BY SIMILARITY.
EXTRACELIGIAR (BY SIMILARITY)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 -NDQQDRDGN-----GDRAESWAVGAKYDANNVYLAAVYAETRN 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 KNNYIVSDSNGYWNWKGANPEDWIEGAAVAAKQDYPGVVNDTTKD 234
EXTRACELLULAR (BY SIMILARITY)
                                                                                                                                                                ; Pred. No. 1.5;
28; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venegas A., Gomez I., Bruce E., Martinez M.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                              D -> G (IN REF. 1).
F5059B37EA516859 CRC64;
                                                                                                                                                                                                                                                                                  56 ---NRAIDIMSRNTTIVNPNETALLNEW----RADLENG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 AA
                                                                                                                                                  6.4%; Score 97.5;
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                                                                                                                                                                    23.5%;
                                                                                                                                                                  Best Local Similarity 23.5
Matches 67; Conservative
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   312
324
326
336
353
363
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                                                                                                                   363 AA;
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P37432;
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28-FEB-2003
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   DOMAIN
TRANSMEM
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SADYENPY---YDNSTY---ASHFYDPDTGTTYIPFAKHAKETGAKYFNLAGQAYQNQDM 143
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EMBL, D90707, BAA35329.1; ALT_INIT.
PIR; H64802; H64802.
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97061202; PubMed=8905232;
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                                                                                                                                                                                Created)
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS00576; GRAM_NEG_PORIN; 1.
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InterPro; IPR001702; Porin Gram-ve.
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EMBL; AE008743; AAL19933.1; -
PIR; S43159; S43159.
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StyGene; SG10264; ompF.
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                                                                                            144 QQAFFYL--GLS--LHYLGDVNQPMHAANFTN---LSYPM-----GFHSKYENFVDTI 189
                                                                                                                                            164 ---FFGLVDGLSFGIQYQGK-NQDNHSINSQNGDGVGYTMAYBFDGFGVTAAYSNSKRT- 218
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SIDYGRNYGIVYDVESYTDMAPYPSGETWGGAYTDNYMTSRAGGL-----LTYRNSD-
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Man B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                                                                                                                                                                         219 -NDQQDRDGN-----GDRAESWAVGAKYDANNVYLAAVYAETRN 256
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                                                                                                                                                                                                                                                          KNNYIVSDSNGYWNWKGANPEDWIEGAAVAAKQDYPGVVNDTTKD
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Hypothetical protein, Complete proteome.
SEQUENCE 468 AA, 52780 MM, 954B5A778AEIC2E4 CRC64,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                   231 KNNFVLEAAFGQAEGYIDQYFAKASYKPDIAGSPLTTSYQFYGTRDKVDDRSVNDLYDGT 290
                                                           LSHSTWNANLDFQSGYAADMFGLDIAAFTAIEMAENGDSSHPNEIAFSKSNKAYDEDWSG 126
                                                                                                                                                                                                     LAGO---AYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANFTNLSYPMGFHSKYENFVDTI 189
                                                                                                                                             DLENGI--YSADYENPYYDNSTYASHFYDPDTGTT-----YIPFAKHAKETGAKY-FN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNNYIV----SDSNGYMN--WKGANPEDWIEGAAVAAKQDYPGV-----VNDTTKD- 234
INSHLWIVNR------AIDI------MSRNTTIVNPNETALL-----NEWRA 82
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(1245); P8981;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Oxystearol-binding protein homolog 2.
Oxystearol-binding protein homolog 2.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycerales; Saccharomycetes;
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
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MEDLINE=21301806; PubMed=11408574;
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GermOnline; 140261; -
8GD; $0002177; OSH2.
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1002 -----PPISATWIE-SPRWDFWG--ESFVDTKFNGRSFNVKHLGLWHIKLRPNDNEKEE 1052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 LGDVNQPMHAANFTNLSYPMGFHSKYENFVDTIKNNYIVSDSN-GYWN-----
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GO; GO:0005935; C:bud neck; IDA.
GO; GO:0005886; C:plasma membrane; IDA.
GO; GO:0006694; P:steroid biosynthesis; IGI.
                                                          InterPro; IPR002110; ANK.
InterPro; IPR000648; Oxysterol_BP
InterPro; IPR001849; PH.
                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
SEQUENCE
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Search completed: July 27, 2004, 14:46:31 Job time : 15 secs

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Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides.
                                                                                                                                                                                                                                                                                                             Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                              (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-010914/01.
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                                                                                                                                                                                                                                   ABB47676;
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Abu01020 S. pneumo
Abu45746 Protein e
Abu68020 Novel hum
Aag68288 Modlfied
Abu86828 B. atero
Abu86828 B. atero
Abu86828 Brevibaci
Abu5230 Protein B
Aag52327 Arabidops
Aag55009 Arabidops
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Aar52563 Clostridi
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1 MKKKVLALAAMVALAAPVQS........EAQRVTAGYIHLWFDTYVNR 282
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5.1.6
Compugen Ltd.
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                                                                                                                                          1586107 seqs, 282547505 residues
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GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                  Minimum Match 0%
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Listing first 45 summaries
                                 OM protein - protein search, using sw model
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ABU08981
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Protein e	Abu19765	ABU19765	ø	584	5.9	90.5	44
Bifidobac	Abp65417	ABP65417	ß	449	5.9	90.5	43
•	Aag05829	AAG05829	m	296	5.9	90.5	42
-	Aag50135	AAG50135	m	296	5.9	90.5	41
	Aag52328	AAG52328	m	165	5.9	90.5	40
	Aag05010	AAG05010	٣	165	5.9	90.5	39
_	Abm67131	ABM67131	9	238	6.0	91.5	38
Novel hum	Abg01338	ABG01338	4	1984	0.9	92	37
	Aaw83352	AAW83352	0	304	6.1	92.5	36
Seed stor	Aaw85564	AAW85564	0	304	6.1	92.5	.35
Amaranthu	Aaw34599	AAW34599	N	304	6.1	92.5	34
	Aay81710	AAY81710	m	2120	6.1	93	33
	Aab48342	AAB48342	4	664	6.1	93	32
Staphyloc	Abm72521	ABM72521	9	370	6.1	93	31
	Abu27268	ABU27268	9	787	6.1	93.5	30
	Abg30886	ABG30886	ß	479	6.1	93.5	29
Clostridi	Aay70519	AAY70519	m	837	6.2	94	28
_	Aaw93146	AAW93146	7	399	6.2	94	27
Aag10304 Arabidops	Aag10304	AAG10304	٣	.346	6.2	94	26

ALIGNMENTS

Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease. Listeria monocytogenes protein #380 ABB47676 standard; protein; 289 AA 11-APR-2001; 2001WO-FR001118. 11-APR-2000; 2000FR-00004629

Dehoux P; Cossart P; Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart E Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charlin A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N, Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J; Rose M, Voss H;

Claim 6; SEQ ID NO 381; 192pp; French.

of L The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments it are useful for selecting probes and primers for detecting genes in monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins

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gene therapy; vaccine
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(GENO-) INST GENOMIC
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                                                                                                                   Sequence 370 AA;
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11-FEB-2003
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      antibodies, identification of L. monocytogenes and related organisms, and for blosynthesis and biodegradation, especially biosynthesis of Vitamin Sells. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccinas compositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIND at
                                                                                                                                                                                                                                                   SHIMIVNRAIDIMSRNTIIVNPNETALLNEWRADLENGIYSADYENPYYDNSTYASHFYD 109
                                                                                                                                                                                                                                                                                                                                        170 INLSYPMGFHSKYENFVDTIKNNYIVSDSNGYMNWKGANPEDMIEGAAVAAKQDYPGVVN 229
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                                                                                                                                                                                                                                                                2 KKKVLALAAMVA-LAAPVQSVV-----FAQT----NNSESPAP-ILRWSAEDKHNEGIN
                                                                                                                                                                                                                      110 PDTGTTYIPFAKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANF
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptides from C-terminus of Clostridium perfringens alpha toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha-toxin; AT; gas gangrene; vaccine; bacterium; Cpa; conjugate; phospholipase C; sphingomyelin-hydrolysis.
 expressed from the genome sequence are useful for raising specific
                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                    230 DITKDWFVKAAVSQEYADKWRAEVTPVTGKRLMEAORVTAGYIHLW 275
                                                                                                                                                                                                                                                                                                                                                                                                  244 AKTKKSYLVG-----NSEWKKDTVEPTGARLKDSQQTLAGFLEFW 283
                                                                                                                                                             Length 289;
                                                                                                                                                             / Match 33.6%; Score 511; DB 5; Length 28; Local Similarity 37.1%; Pred. No. 5.7e-39; nes 106; Conservative 55; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium perfringens alpha-toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR52563 standard; protein; 370 AA.
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92GB-00015655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
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                                                                                                                                           Sequence 289 AA;
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23-JUL-1992;
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30-MAY-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 EGINSHLWIVNRAIDIMSRNTTIVNPNET----ALLNEWRADLENGIYSADYENPYYDNS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .02 TYASHFYDPDTGTTYIP----FAKHAKETG----AKYFNLAGQAYQNQDMQQAFFYLGL 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 LYQDHFWDPDTDNNFSKDNSWYLAYSIPDTGESQIRKFSALARYEWQRGNYKQATFYLGE 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antinflammatory; antibacterial; immunostimulant; auditory; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                     Peptides, or conjugates, have the amino acid sequence of the epitopes of C. perfringens alpha-toxin (AT) from amino acids 261-300 but lack phospholiphase C and/or sphingomyelin-hydrolysing activity. The peptides induce a protective immune response against AT when admin. to human or animals. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 SLHYLGDVNQPMHAANFTNLSYPMGFHSKYENFVDTIKNNYIVSDSNGYWN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----WKGANPEDWIEGAAVAAKODYPGVVNDTTKDWFVKAAVSQEYAD-KWRAEVTPV
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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useful in protective vaccines against gas gangrene, also derived antibodies for passive immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                      54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S. pneumoniae type 4 strain protein from coding region #590.
                                                                                                                                                                                                                                                                                                                                                                            Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                      95, Indela
                                                                                                                                                                                                                                                                                                                                                                         14.5%; Score 220; DB 2; 26.5%; Pred. No. 1.1e-11; iive 40; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae; type 4 strain.
                                                                                           Disclosure; Page 16-17; 29pp; English.
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----LANSQKGTAGYIY 237
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                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 26.55.
Local Similarity 26.55.
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(first entry)
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19-JUN-2003 (first entry)

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Streetcoccus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, Creating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target composition primer is substantially complementary to the target sequence the first primer is substantially complementary to the complement of the target sequence, and where the parts of the primers having the target sequence. The target sequence complementarity define the termini of the target sequence or substantial complementary to the complement of the target sequence, and where the parts of the primers having substantially complementary to the complement of the target sequence or substantial complementarity define the termini of the target sequence or substantial complementarity define the termini of the target sequence or substantial complementarity define the termini of the target sequence or protein, and determining whether the test compound binds to the protein and a Streptcocccus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, nucleic card and addisected in an encoding the proteins are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful as genenic sequence. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic forma directly from wire an effect on the present sequence (Updated on 23-0CT-2003 to
   streptococcus bacteria, such as pneumonia, sepsis, otitis media or
                                                                                                                                                   The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the
                                                                                         Claim 1; SEQ ID NO 1180; 56pp; English
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66 Indels 39; Mismatches 109; DB 6; Score 108.5; I Pred. No. 3.3; 7.1%; Query Match
Best Local Similarity 23.8% Sequence 2140 AA;

1 MKKKV---LALAAMVALAAPVQSVVFAQTNNSESPAPI--LRWSAEDKH-NEGINSHL-- 52

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97 YYDNSTYASHFYDPDTGTTYIPFAKHAKETGAKY----FNLAGQAYQ----NQD---- 142
                                                                                                                                                               121 KEDKVVYIAEFKDKESGEKAIKELSSLKNTKVLYTYDRIFN--GSAIETTPDNLDKIKQI 178
                                                                                                                                                                                                      ----MOOAFFYLGL--SLHYLGDVNQPMHAANF-----TNLSYPMGF 178
                                                                                                                                                                                                                                                                                      HSKYENFVDTIK------NNYIVSD----SNGYWNWKGANPEDWIEGAAVAA 220
  9
                                         ------WIVNRAIDIMSRNTTIVN--PNETALLNEWRADLENGIYSADY-----ENP- 96
                                                                                                                                                                                                                                                                                                             RHKAMRIDDDAKASMRFKKEDLKGTDKNYWLSDKIPHAFNYYNGGKITVEKYDDG----
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ABU45746 standard; protein; 2140 AA.
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the invention fractates to an interest acts comparisons of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antiennse
concleic acid; (2) a host cell containing the vector; (3) an isolated
cucleic acid; (4) an antibody capable of specifically binding
cutisense nucleic acid; (4) an antibody capable of specifically binding
cut the polypeptide; (5) producing the polypeptide; (6) inhibited by the
control or the activity of a gene in an operon required for
proliferation or that has an activity against a biological pathway
control or that has an activity against a biological pathway
control or that has an activity against a biological pathway in which a proliferation-required gene or its gene product lies
congounds activity; (1) actual or the biological pathway in which a proliferation-required gene or its gene product lies
correctly a gene required for cellular proliferation of an
corganism acts; (9) manufacturing an antibiotic; (10) profilling a
compound's activity; (11) a culture comprising strains in which the gene
product is overexpressed or underexpressed; (12) determining the extent
confounds; or (13) identifying the target of a compound that inhibits the
confounds; or (13) identifying the target of a compound that inhibits the
confounds activity; (1) a culture conquise for inhibits confection of
confounds; or (13) identifying the target of a compound that inhibits the
confounds activity; or conference or collection of
confounds or corresponsed or underexpressed; (12) determining the extent
confounds or collection of an organism. The antisense nucleic acids required
confounds or screening for homologous nucleic acids required
confounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at
                                                                                     Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   relates to an isolated nucleic acid comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohlsen KL,
Forsyth RA,
                                         Protein encoded by Prokaryotic essential gene #31273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; SEQ ID NO 73670; 1766pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                        21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                            21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAR-2002; 2002US-0362699P
                                                                                                                                        Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zamuđio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2003-029926/02.
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Wall |
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Gaps

99;

Indels

; Score 108.5; DB 6; ; Pred. No. 3.3; 39; Mismatches 109;

23.8%;

Best Local Similarity 23.8% Matches 77; Conservative

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Length 2140;

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31-MAY-2001,
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                                                                                                                                                                                                                                                                                                                                                        398
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                                                                                                                                                 Query Match
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                                                 SQDFKEKKTAVIKEKEVVSKNPVIDNNTSNBEAKIKEENSNKSQGDYTDSFVNKNTENPK 120
                                                                                YYDNSTYASHFYDPDTGTTYIPFAKHAKETGAKY----FNLAGQAYQ----NQD----- 142
                                                                                               121 KEDKVVYIAEFKDKESGEKAIKELSSLKNTKVLYTYDRIFN--GSÅLETTPDNLDKIKOI 178
                                                                                                                                                                       179 HSKYENFVDTIK------NNYIVSD----SNGYWNWKGANPEDWIEGAAVAA 220
                                                                                                                                                                                     238 RHKAMRIDDDAKASMRFKKEDLKGTDKOYWLSDKIPHAFNYNGGKITVEKYDDG---- 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used genes. (I) is useful in gene therapy techniques to rescore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of altes expressing (II). (I) are useful for treating disorders
96
                                     -----WIVNRAIDIMSRNTTIVN--PNETALLNEWRADLENGIYSADY-----ENP-
                                                                                                                           ------TNLSYPMGF
                                                                                                                                                 179 EGISSVERAQKVQPMMNHARKEIGVEEAIDYLKSINAPF-GKNFDGRGMVISNIDTGTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID NO 38749; 103pp; English.
                                                                                                                                                                                                                     234
                                                                                                                                                                                                                                 :|| :| | :: | 293 -RDYFDPHGMHIAGILAGNDTEQD 315
                                                                                                                                                                                                                                                                                                                                                                  Novel human diagnostic protein #8381.
                                                                                                                                                                                                                                                                                                ABG08390 standard; protein; 444 AA
                                                                                                                                                                                                                   221 KQDY------PGVV--NDTTKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT;
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2000US-00649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 TYIPPAKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLHYLGDVN----QPMHAANFT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moss; Physcomitrella patens; lipid metabolism related protein; LMRP; lipid blosynthesis; lipid modification; lipid degradation; cofactor; fatty acid transport; genetic engineering; fatty acid; enzyme; plant; microorganism; polyunsaturated fatty acid; oliseed plant; maize; wheat; biotic stress tolerance; abiotic stress tolerance; rye; oat; triticale; rice; bartey; soybean; peanut; octton; rapseed; canola, manihor; pepper; sunfilower; tagetes; potato; tobacco; eggplant; cometo; Vicia; pea; alfalfa; coffee; cacao; tea; Salix; oil palm; coconut; perennial grass;
involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic mains acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed appecification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 AIDIMSRNTTIVNPNE---TALLNEWRADLENGIYSADYENPYYDNSTYASHFYDPDTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KKKVIALAAMVA----LAAPVQSVVFAQTNNSESPAPILRWSAEDKHNEGINSHLWIVNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Psychomitrella patens useful to produce fine chemicals in modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52;
                                                                                                                                                                                                                                                                                                                                                                                                                6.6%; Score 100; DB 4; Length 444; 22.3%; Pred. No. 2.1; tive 36; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      д, <del>Ц</del>
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Schmidt R,
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Duwenig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 22.33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Physcomitrella patens.
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Freund A,
                                                                                                                                                                                                                                                                                                                                                        Sequence 444 AA;
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                                        The present invention describes isolated nucleic acid sequences which encode lipid metabolism related proteins (LMRP). The LMRP nucleic acids encode lipid metabolism related proteins (LMRP). The LMRP nucleic acids man be used to modify lipids and fatty acids, cofactors and enzymes in microorganisms and plants, particularly to produce polyunsaturated fatty acids, and are especially useful in oilseed plants. The nucleic acids may also confer biotic or abiotic stress tolerance, particularly to maize, wheat, rye, oat, triticale, rice, barley, soybeaut, portion, rapeseed, canola, manihot, pepper, sunflower, tagetes, potato, tobacco, eggplant, tomato, vicia species, pea, alfalfa, coffee, cacao, tea, Salix species, oil palm, coconut, perennial grasses and forage crops. AAH50878 to AAH50882 represent primers used in the exemplification of the present invention. AAH5082 represent LMRP protein sequences, and
                                                                                                                                                                                                                                                                                                            231
                                                                                                                                                                                                                                                                                                                                  NGIYSADYENPYYDNSTYASHFYDPDTGTTYIPFAKHAKETG-AKYFNLAG-QAYQNQDM 143
                                                                                                                                                                                                                                                                                                                                                                                             : |: : : : : : | : ENAYTKIVEKLFEIDPDGAMLAFADMMRKKISMPAHLMYDGQNDHLFDDFSLVAQRTG-- 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brevibacillus laterosporus; insecticidal secreted protein; ISP1A; ISP2A; ISP1A-1; ISP2A-1; toxin; bacterial; plant protection.
organisms, particularly polyunsaturated fatty acids in oilseed plants.
                                                                                                                                                                                                                                                                                                   NNPYLGFVYTSFQERATFISH-----GNT----ARHAKEHGDAKLATICGIIAADERRH
                                                                                                                                                                                                                                                                                      31 SPAP----ILRWSAED-KHNEGINSHLWIVNRAIDIMSRNTTIVNPNETALLNEWRADLE
                                                                                                                                                                                                                                                                                                                                                                                QQAFFYLGLSLHYLGDVNQPMHAANFTNLSYPMGFHSKYENFVDT1KNNY-1VSDSNGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                          NWKGANPEDWIEGAAVAAKQDYPGVVNDTTKDWFV------KAAVSQEY 245
                                                                                                                                                                                                                                        6.4%; Score 98; DB 4; Length 414; 21.6%; Pred. No. 2.9; ive 39; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Van Rie J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified ISP1A-1 protein SEQ ID NO:10.
                     Page 118; 120pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG68288 standard; protein; 836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-MAY-2000; 2000US-00573872.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brevibacillus laterosporus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-062371/08
N-PSDB; ABA04061.
                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                              present invention
                                                                                                                                                                                                                    Seguence 414 AA;
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                     Claim 31;
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                                                                                                                                                                                                                                                                                                                                  98
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Matches
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14;
                                                                                                                                                                                                       The present invention describes 2 Brevibacillus laterosporus insecticidal secreted proteins designated ISP1A and ISP2A. ISP1A, and ISP2A, are insecticidal to Diabrotica virgifiera larvae when ingested by larvae in combination with the ISP2A amino acid sequence 51 to 457, or ISP1A amino acid sequence 51 to 457, or ISP1A amino controlling insects. The polymucleotide sequences encoding ISP1A and ISP2A can be used in the production of transgenic plants resistant to coleopteran insects. The present sequence represents a modified ISP1A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .2
/note= "The wild-type signal peptide (amino acids 1-37 of
ABU08981) have been substituted by Met-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 SFGVSVNYQHSETVANEWGSAINDGTHINGAESAYLNANVRYNNVGTGAIYETKPTTSFI 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --GTTY1PFAKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANFT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        432 QLNTYLSNKKPILLETDQVEGKYAIKDTNGNITIAGDWNGITDEISAKTASIIVDNGNQM 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----AAKQDYPGVVNDTTKDWFVKAAVSQEYADKWRAEVTPVTGKRLMEAQRVTAGYIHL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     492 SEKRVAAKDYIN-PEDKIPNLSVKKAALKLAYPD----EIEBKDGLLFYNDQPIFEASVQS 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insecticidal secreted protein; toxin; ISP2A; insecticide; Diabrotica sp; Leptinotarsa sp; Anthonomus sp; corn; coleopteran insect; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAAFPSVNVSLEKVILSKNEDLSHSVESSQSTNWSY -- TNTEGVN----- VNAGWSGLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRNTTIVNPNETALLNEWRADLENGIYSADYENPY----YDN-STYASHFYDPDT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 NLSYPMGFHSKYENFVDTIKNNYIVSDSNG----YWNWKGANPEDWIEGAAV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAAMVALAAPVQSVVFAQT ---NNSESPAPILRWSAEDKHNEGINSHLWIVNRAIDIM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
New bacterial insecticidal proteins, useful for making insecticidal composition to protect plants from damage by insects especially coleopteran insects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B. laterosporus truncated insecticidal secreted protein, ISPIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 96.5; DB 5; Length 8; Pred. No. 11; 48; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3. .836
/label= Mature_ISP1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                            Claim 4; Page 82-86; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU08984 standard; protein; 836 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brevibacillus laterosporus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 21.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 WFDTY 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 836 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002199215-A1
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The present sequence represents a Brevibacillus laterosporus insecticidal secreted protein designated ISP1A. ISP1A, and ISP2A, are insecticidal to Diabrotica virgifera larvae when ingested by larvae in combination with the ISP2A amino acid sequence 51 to 457, or ISP1A amino acid sequence 51 to 457, or ISP1A amino acid sequence 38 to 811, respectively. ISP1A and ISP2A are useful for controlling insects. The polynucleotide sequences encoding ISP1A and ISP2A can be used in the production of transgenic plants resistant to coleopteran insects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 SRNTTIVNPNETALLINEWRADLENGIYSADYENPY----YDN-STYASHFYDPDT--- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      492 SEKRVAAKDYIN-PEDKIPNLSVKEALKLAYPD----BIBEKDGLLFYNDQPIFEASVQS 546
              ----AAKQDYPGVVNDTTKDWFVKAAVSQEYADKWRAEVTPVTGKRLMEAQRVTAGYIHL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brevibacillus laterosporus; insecticidal secreted protein; ISP1A; ISP2A; ISP1A; ISP2A; ISP1A-1; ISP2A-1; toxin; bacterial; plant protection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 VAAFPSVNVSLEKVILSKNBDLSHSVESSQSTNWSY--TNTBGVN-----VNAGWSGLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAAMVALAAPVQSVVFAQT---NNSESPAPILRWSAEDKHNEGINSHLWIVNRAIDIM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New bacterial insecticidal proteins, useful for making insecticidal composition to protect plants from damage by insects especially coleopteran insects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brevibacillus laterosporus ISPIA protein SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.3%; Score 96.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van Rie J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 61-65; 86pp; English.
                                                                                                                                                                                                                                                                                                                  AAG68285 standard; protein; 871 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .37
/label= signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AVET ) AVENTIS CROPSCIENCE NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Damme N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38. .871
/label= ISP1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-2000; 2000US-00573872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAY-2001; 2001WO-EP005702.
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                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-062371/08.
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Best Local Similarity
                                                                                                                         275 WFDTY 279
                                                                                                                                                                               551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABA04056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 871 AA;
                                                                                                                                                                 : | |
547 YVDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200187931-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a new insecticidal secreted protein comprising:

(a) amino acid sequence of the smallest active toxin of the protein

(b) the amino acid sequence appearing as ABU08981 (ISB1A);

or (b) the amino acid sequence of the protease-digestion fragment of the

protein encoded by the insecticidal secreted protein (isp) and isp2A);

or (b) the amino acid sequence of the protease-digestion (isp2A);

or (c) the amino acid sequence accession number IMBP 4009. Also

included are a DNA sequence encoding the protein (isp3) and isp2A DNA

comprising the DNA and a plant-expressible promoter region (e.g. the

comprising the bund a plant-expressible promoter region (e.g. the

comprising the chimaeric gene bromoter), a plant cells

comprising the chimaeric gene of integrated in its cells,

a microorganism transformed to contain the DNA encoding ISP1A, or ISP2A, a

controlling insects comprising expressing a plant resistant to

coleopteran insects (comprising transforming plant cells with a first

coleopteran insects (comprising transforming plant cells with a first and

coleopteran insect genes are ISP1A and ISP2A, and a process for controlling

coleopteran insect peace (comprising planting, sowing or growing in a

coleopteran insect peace with a first and second chimaeric gene are ISP1A and ISP2A, and a process for controlling

coleopteran insect peace with a first chimaeric gene are ISP1A and

coleopteran insect peace are ISP1A and ISP2A, and a process for controlling

coleopteran insect peace (insect of planting) and second

chimaeric gene, where the first and second chimaeric gene are ISP1A and

coleopteran insect coleopteran insect (e.g. Diabricing, sowing or growing in a

coleopteran insect peace are ISP1A and ISP2A, and a process for controlling

coleopteran insect beated proteins and second

chimaeric gene, where the first and second chimaeric gene are ISP1A and

coleopteran insecticidal secreted proteins and NA second chimaeric gene are ISP1A and

coleopteran insecticidal secreted protein cured by i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRNTTIVNPNETALLARWRADLENGIYSADYENPY----YDN-STYASHFYDPDT--- 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380 LDGTT-İGTIK-AKENTTALTILPDQSYPEKGKN-----ĞIAINTMDDFNSRPIPLNKE 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 NLSYPMGFHSKYENFVDTIKNNYIVSDSNG----YWNWKGANPEDWIEGAAV----- 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             432 OLNTYLSNKKPILLETDQVEGKYAIKDTNGNITIAGDWNGITDEISAKTASIIVDNGNQM 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 LAAMVALAAPVQSVVFAQT---NNSESPAPILRWSAEDKHNEGINSHLWIVNRAIDIM-- 62
                                                                                                                                                                                                                                                                                                                                                                                                                           New insecticidal secreted proteins and DNA sequences, useful in making insecticidal compositions or transgenic plants to protect plants from damage caused by insects, particularly coleopteran insects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 --GTTYIPPAKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.3%; Score 96.5; DB 6; Length 836;
21.0%; Pred. No. 11;
:ive 48; Mismatches 140; Indels 53
                                                                                                                                                                                                                                                                                                 Damme N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 32-34; 38pp; English.
                                                                                                                                                                                                                                                                                              Rie JV,
                                                17-MAY-2001; 2001US-00858525
                                                                                                      17-MAY-2001; 2001US-00858525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64; Conservative
                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-361872/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                              Boets A, Arnaut G,
                                                                                                                                                      (BOET/) BOETS A. (ARNA/) ARNAUT G. (RIEJ/) RIE J V. (DAMM/) DAMME N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 836 AA;
                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABX94353
26-DEC-2002
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included are a DNA sequence encoding the protein cited above, a chimaeric gene comprising the DNA and a plant-expressible promoter region (e.g. the long and short forms of the corn zrp2 gene promoter), a plant cell.

Comprising the chimaeric gene used to produce the protein cited above, a plant or a seed comprising the chimaeric gene by produce the protein cited above, a microorganism transformed to contain the DNA encoding ISPIA, a process for controlling insects comprising expressing the protein cited above in cells of a plant, a process for rendering a plant resistant to coleopteran insects (comprising transforming plant cells with a first chimaeric gene and a second chimaric gene, and regenerating transformed plants from the cells which are resistant to insects, where the first and second chimaeric gene are ISPIA and ISPIA, and a process for controlling coleopteran insect pests (comprising planting, sowing or growing in a field plants transformed with a first chimaeric gene and a second chimaeric gene, where the first and second chimaeric gene, where the first and second chimaeric gene are ISPIA and ISPIA, and ISPIA, the insecticidal secreted proteins and bNA sequences are useful in making insecticidal compositions or transgenic plants to protect plants (especially crops like corn) from damage caused by insects particularly coleopteran insects (e.g. Diabrostica sp. Diabrostica sp. cand Anthonomus sp.). The proteins are useful for preventing or minimising insectic damage to plants in a field. The present sequence represents ISPIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --GTTYIPFAKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANFT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415 LDGTT-IGTIK-AKENTTALTILPDQSYPEKGKN-----GIAINTMDDFNSRPIPLNKE 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 ----AAKQDYPGVVNDTTKDWFVKAAVSQEYADKWRAEVTPVTGKRLMEAQRVTAGYIHL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 527 SEKRVAAKDYIN-PEDKIPNLSVKEALKLAYPD----EIEEKDGLLFYNDQPIFEASVQS 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRNTTIVNPNETALLNEWRADLENGIYSADYENPY----YDN-STYASHFYDPDT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 NLSYPMGFHSKYENFVDTIKNNYIVSDSNG----YWNWKGANPEDWIEGAAV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 QLNTYLSNKKPILLETDQVEGKYAIKDTNGNITIAGDWNGITDEISAKTASIIVDNGNOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 LAAMVALAAPVQSVVFAQT---NNSESPAPILRWSAEDKHNEGINSHLWIVNRAIDIM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6; Length 871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 96.5; DB 6; Length 87; Pred. No. 12; 48; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multiprotein complex; eukaryote; drug target; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABR52701 standard; protein; 1283 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 6.3%;
Local Similarity 21.0%;
Les 64; Conservative 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-DEC-2001; 2001EP-00130253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein sequence #SEQ ID 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 WPDTY 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 871 AA;
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582 YVDEY
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Matches
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(a) amino acid sequence of the smallest active toxin of the protein comprising a sequence appearing as ABU08981 (ISP1A) or ABU08982 (ISP2A); or (b) the amino acid sequence of the protease-digestion fragment of the protein encoded by the insecticidal secreted protein (isp)1A or isp2A DNA deposited at the BCCM-LMBP under accession number LMBP 4009. Also
                                                         ----AAKQDYPGVVNDTTKDWFVKAAVSQEYADKWRAEVTPVTGKRLMEAQRVTAGYIHL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38. .768
/label= Active fragment
/note= "This protein is specifically claimed in claim 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secreted protein; toxin; ISP1A; insecticide; Diabrotica sp; Bp; Anthonomus sp; corn; coleopteran insect; transgenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Mature_ISP1A
/note= "This protein is specifically claimed in claim 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New insecticidal secreted proteins and DNA sequences, useful in making insecticidal compositions or transgenic plants to protect plants from damage caused by insects, particularly coleopteran insects.
                                                                                                                                                                                                                                          SEKRVAAKDYTN-PEDKTPNLSVKEALKLAYPD----EIEEKDGLLFYNDQPIFEASVQS
                                                                                                                                            |: : | : |: |: | OLATYLSNKKPILLETDQVEGKYAIKDTNGNITIAGDWNGITDEISAKTASIIVDNGNQM
                               --GITYIPFAKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANFT
                                                                                                                  NLSYPMGFHSKYENFVDTIKNNYIVSDSNG----YWNWKGANPEDWIEGAAV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B. laterosporus insecticidal secreted protein, ISP1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .37
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Damme N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU08981 standard; protein; 871 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 18-20; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rie JV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-MAY-2001; 2001US-00858525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boets A, Arnaut G,
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582 YVDEY 586
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ARNAUT G.
RIE J V.
DAMME N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABX94348
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Leptinotarsa
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                                                                                                                                                             467
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(DAMM/)
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Gaps

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9908-0121825P.
9908-0125788P.
9908-0126764P.
9908-0126764P.
9908-0126734P.
9908-0128734P.
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99US-0139750P.
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                                                     25-FEB-2000; 2000EP-00301439.
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01-APR-1999;
06-APR-1999;
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           EP1033405-A2
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                                 06-SEP-2000
944 TFEDSTLRTLYVAAFTASSYASTTKRV-AKPFNPLLGETFEYSRPDKQYRFFTEQVSHH- 1001
                                                                                                                                                                                                          The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52568-ABR53903 and ACC6610-ACC6144 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a plarmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this parent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete document is available on CD-ROM
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---LWIVNRAI---DIMSRNTTIVNPNE-TALLNEWRADLENGIYSADYENPYYDNSTYAS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 HFYDPDTGTTYI-----PFAKHAKETGAKYFN-LAGQA--YQNQDMQQAFFYLGLSLHY 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 LGDVNQPMHAANFINLSYPMGFHSKYENFVDTIKONYIVSDSN-GYWN----- 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKKVLALAAMVALAAPVQSVVFAQTNNSESPAPILRWSAEDKHNEGINSH------ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein identification, signal transduction pathway, metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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                                                                                                                             New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease disorder.
                                                                                                                                                                                                                                                                                                                                                                                          Match 6.3%; Score 95.5; DB 6; Length 1283; Local Similarity 25.9%; Pred. No. 26; Conservative 31; Mismatches 104; Indels 71;
                                                         Kruse UD, Kuester BD;
                                                                                                                                                                                        Disclosure; SEQ ID NO 267; 17pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 66504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1053 LYTWK--KPNNTVIGILIGNPQVDNHGEVNVVNHTTGD 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---WKGANPEDWIEGAAVAAKQ-DYPG---VVNDTTKD 234
                                                           Bauer A, Gavin A, Grandi P, Krause R, K
Marzioch M, Schultz JD, Superti-Furga GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG52327 standard; protein; 192 AA
                15-MAY-2001; 2001EP-00111774.
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                                                                                               WPI; 2003-250078/25.
                                      (CELL-) CELLZOME AG
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23-AUG-1999;
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13-SEP-1999;
15-SEP-1999;
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GOAYONODMOOAFFYLGLSLHYLGDVNOPMHAANFTN-----LSYPMGFH---- 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REIILTALKENYDKNLDLLQEDLEKNITNGLWHDDLSSWTECNDLIACPHKYASESIKLA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTSDRRYNWTEALLFLS---HFMGDIHQPMH-VGFTSDEGGNTIDLRWYKHKSNLHHVWD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | | | : | | : | | : | CKWGYKGVKSGET-----LSEEYPN----TRLPIVMKRIVQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 AKQDYPGVVNDTTKDWFVKAAVSQEYADKWRAEVTPVTGKRLME 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 1251.
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21.3%; Pred. No. 2;
ive 29; Mismatches
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                  9905-01547799-
9905-01551399-
9905-01556389-
9905-01556389-
9905-01573129-
9905-01573129-
9905-0157329-
9905-01592319-
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tes 35; Conserv
16-SEP-1999,
22-SEP-1999,
23-SEP-1999,
24-SEP-1999,
28-SEP-1999,
29-SEP-1999,
06-OCT-1999,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SKYENFVDTIKNNYIVSDSNGYW----NWKGAN----PEDWI-EGAAVA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 REIILTALKENYDKNLDLLQEDLEKNITNGLWHDDLSSWTECNDLIACPHKYASESIKLA 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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 990S-0154018P

990S-0154039P

990S-0155139P

990S-0155139P

990S-015563P

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PR 30-JUN-1999; 9910-0140991P: PR 01-JUL-1999; 9910-0140991P: PR 01-JUL-1999; 9910-0140991P: PR 01-JUL-1999; 9910-014091P: PR 01-JUL-1999; 9910-014208P: PR 02-JUL-1999; 9910-014208P: PR 03-JUL-1999; 9910-014208P: PR 13-JUL-1999; 9910-014433P: PR 20-JUL-1999; 9910-014531P: PR
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135 GQAYQNQDMQQAFFYLGLSLHYLGDVNQPWHAANFTN-----LSYPMGFH---- 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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termination sequence
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05-MAR-1999;
03-MAR-1999;
25-MAR-1999;
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01-APR-1999;
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116-APR-1999;
116-APR-1999;
123-APR-1999;
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PR 11-68P-1999) 9908-015376P.
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PR 23-007-1999) 9908-01559P.
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             Sequence 10, Appl
Sequence 11, Appli
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Sequence 2, Appli
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Sequence 2785, Ap
Sequence 13140, A
Sequence 1785, Ap
Sequence 559, App
Sequence 569, App
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US-09-503-311-14

US-09-503-311-13

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Patent No. 5817317
GENERAL INFORMATION:
APPLICANT: TITBALL DR, RICHARD W
APPLICANT: WILLIAMSON DR, ETHEL D
TITLE OF INVENTION: CLOSTRIDIUM PERFRINGENS VACCINES
NUMBER OF SEQUENCES: 4
CORRESPONDENCES:
ADDRESSEE: NIXON & VANDERHYE
STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: PLOPS MS-DOS
SOFTWARE: PATENTINE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTINE DATA:
APPLICATION NUMBER: US/08/341,538A
FILING DATE: 28-NOV-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: GB 9210717.6
FILING DATE: 20-MAY-1992
RIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9215655.3
FILING DATE: 23-JUL-1992
RIOR APPLICATION NUMBER: WO GB93/01039
FILING DATE: 20-MAY-1993
ATTONEY/AGENT INPOMBER: WO GB93/01039
FILING DATE: 20-MAY-1993
ATTONEY/AGENT INPOMBATION:
NAME: CRAWFORD ARTHUR R
REGISTRATION NUMBER: 25327
RECRAWFORD ARTHUR R
REGISTRATION NUMBER: 25327
US-09-426-072-2
US-09-428-10-32A-2
US-09-483-101-14
US-09-483-101-14
US-09-134-000C-3519
US-09-134-001C-5389
US-09-134-001C-5389
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US-09-134-001C-5389
US-08-915-136-20
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US-08-915-136-20
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US-08-405-496A-20
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STATE: VIRGINIA
COUNTRY: UNITED STATES
ZIP: 22201-4714
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Matches 68; Conservative
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Pred. No. 6.8e-14;
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APPLICANT: TITBALL DR, RICHARD W
APPLICANT: TITBALL DR, RICHARD W
APPLICANT: WILLIAMSON DR, ETHEL D
TITLE OF INVENTION: CLOSTRIDIUM PERFRINGENS VACCINES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDENYE
ADDRESSEE: NIXON & VANDENYE
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GOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,518
FILING DATE: 4-0CT-96
CLASSIFICATION NUMBER: US 08/341538
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/341538
FILING DATE: 28-NOV-1994
CLASSIFICATION NUMBER: US 08/341538
FILING DATE: 20-MAY-1992
PRIOR APPLICATION NUMBER: US 9210717.6
FILING DATE: 20-MAY-1992
PRIOR APPLICATION NUMBER: US 9215655.3
FILING DATE: 23-JUL-1992
PRIOR APPLICATION NUMBER: WO GB93/01039
FILING DATE: 23-JUL-1993
ATTONING/AGENTING DATE: 20-MAY-1993
ATTONING DATE: 20-MAY-1993
ATTONING/AGENTING DATE: 20-MAY-1993
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STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VINGINIA
COUNTRY: UNITED STATES
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5851827
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REGISTRATION NUMBER: 25327
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26.5%;
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INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 370 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENYDKNLDLLQEDLEKNITNGLWHDDLSSWTECNDLIACPHKYASESIKLACKWGYKGVK 228
                                                                                                                                        .02 TYASHPYDPDIGITYIP-----PAKHAKEIG----AKYFNLAGQAYQNQDMQQAFFYLGL 152
                                           46 EGINSHLWIVNRAIDIMSRNTTIVNPNET ---- ALLINEWRADLENGIYSADYENPYYDNS 101
                                                                                                                                                                       SLHYLGDVNQPMHAANFINLSYPMGFHSKYENFVDTIKNNYIVSDSNGYWN----- 203
                                                                                                                                                                                                                                                                                                                                                                       182 NKDFNAWS----KEYARGFAKTGKSIY------YSHASMSHSWDDWDYAAKVT-- 224
                                                                                                                                                                                                                                                                       ::|| ||:: | | || || : | | || || 1005AGHVKPETFAEERKEQYKINTAGCKTNEAFYTDILK 181
                                                                                                                                                                                                                                                                                                                                      -----WKGANPEDWIEGAAVAAKQDYPGVVNDTTKDWFVKAAVSQEYAD-KWRAEVTPV 256
                                                                         6 DGTGTHAMIVTQGVSILENDLSKNEPESVRKNLEILKENMHELQLGSTYPDYDKNAYD-- 63
54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.3%; Score 96.5; DB 4; Length 276; 21.4%; Pred. No. 0.14; ve 31; Mismatches 67; Indels 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Fox Chase Cancer Center
APPLICANT: Fox Chase Cancer Center
TITLE OF INVENTION: Nucleic Acid Encoding a Mismatch
TITLE OF INVENTION: Endonuclease and Methods of Use Thereof
FILE REPERENCE: 9503dna
CURRENT APPLICATION NUMBER: US/09/510,322A
CURRENT PILLING DATE: 2000-02-22
95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 YASHFY---DPDTGTTYIPFAKHAKETGAKYFNLAGQAYON-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 NDTTKDWFVKAAVSQEYADKWRAEVTPVTGKRLME 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Girardeau, Jean-Pierre
Martin, Christine
Mechin, Marie-Claire
Der Vartanian, Maurice
Bousquet, Francois
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; Patent No. 6096321
; GENERAL INVORMATION:
APPLICANT: Martin, Christine
APPLICANT: Martin, Marie-Claire
APPLICANT: Der Vartanian, Maurice
APPLICANT: Bousquet, Francois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-510-322A-11
; Sequence 11, Application US/09510322A
; Patent No. 6391557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :|: |||||:
----LANSQKGTAGYIY 237
                                                                                                                                                                                                                                                                                                                                                                                                                                         257 TGKRLMBAQRVTAGYIH 273
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Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-510-322A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 276
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USA
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US-09-252-991A-32033
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SUB-UNIT OF CS31A PROTEIN CAPSULE
MODIFIED BY AT LEAST ONE HETEROLOGGOUS PEPTIDE, CS31A
PROTEIN CAPSULE INCLUDING SUCH A SUB-UNIT, AND
MICROORGANISMS WHOSE OUTER MEMBRANE CARRIES SUCH
SUB-UNITS, AND PROCEDURE FOR OBTAINING AND UTILIZING SUCH
SUB-UNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 HLWIVNRAIDIMSRNTTIVNPNETALLNEWRADLENGIYSADYENPYYDNSTYASHFYDP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---FSNTTNEIVKRKLNISVPTDELFLAAKMSDGIKGVFVGNTLIPKIEMASYDGSVITS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DTGTTYIPFAKHAKETG-----LAGGAYQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 PISNIAMDIAVKVKNSGDNTELGTLSVPLSFGAAVTIFDGNTTDSAVAHITSGSÄGTVFE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 N-----QDMQQAFFYLGLS-LHYLGDVNQPMHAANFINLSYPMGFHSKYENFVDTIKN 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 GLVNPGRFTDQNIAYKWNGLSKAEMAGYVEKLMPGKSSTSYS---GFH----NWDDLSHP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |: |: | :: | :: | :: | :----GSGVSAGST---LVMNLNKDVAGRLEWVAPVTITVIY 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --APILRWSAEDKHNEGINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.2%; Score 95; DB 3; Length 274; 21.3%; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,954
FILING DATE: 16-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115;
                                                                                                                                                                                                                                                        SEE: WEISER & ASSOCIATES : 230 South Fifteenth Street, Suite 500 Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKKKVLALAAMVALAAPVQSVVFAQTNNSESP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/01281
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19,763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 98
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 215-875-8383
215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 274 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Weiser, Gerard J
REGISTRATION NUMBER: 19
                                                               TITLE OF INVENTION: PROTITION OF INVENTION: WICH TITLE OF INVENTION: SUB-UNDER OF SEQUENCES: 115 CORRESPONDENCE ADDRESSE: ADDRESSEE: WEISER & ACTION OF INVENTION OF SEQUENCE ADDRESSEE: WEISER & ACTION OF INVENTION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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       INVENTION:
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Matches 64; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 16
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                     STATE: PACOUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ropology:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-491-954-4
                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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RESULT 5 US-08-282-197C-54

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Sequence 32033, Application US/09252991A
Patent No. 5551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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Sequence 54, Application US/08282197C

Patent No. 5871730

GENERAL INFORMATION:
APPLICANT: Brazinski, Ryszard
APPLICANT: Dery, Claude V
APPLICANT: Beaulieu, Carole
TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSERS: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Ave., NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: READABLE FORM:

COMPUTER: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NATA:

APPLICATION NUMBER: US/08/282,197C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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Pred. No.
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NAME: Cimbala, Michele A
REGISTRATION NUMBER: 33,851
REFRENCE/DOCKET NUMBER: 1050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
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1 TYPE: amino acid
1 TOPOLOGY: both
US-08-282-197C-54
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Best Local Similarity 19.78
Matches 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         596 VFTG----TGDGYFKAFDAKSGKELWKFQTGSGIVSPPITWEQDGEQYLGVTVGYGGAV 650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165 HAANFINLSYPMGFHSK--YENFVDTIKNNYIVSDSNGYWNWKGANPEDWIEGAAVAAKQ 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Blum, David L.
APPLICANT: Kataeva, Irina
APPLICANT: Li, Xin-Liang
APPLICANT: Li, Xin-Liang
APPLICANT: Li, Xin-Liang
APPLICANT: Li, Xin-Liang
APPLICANT: Li, Xin-Liang
TITLE OF INVENTION: Phenolic Acid Esterases, Coding Sequences and Methods
FILE REPERINCE: 67-98
CURRENT APPLICATION NUMBER: US/09/390,234
CURRENT FILING DATE: 1999-09-03
EARLIER APPLICATION NUMBER: US 60/099,136
EARLIER APPLICATION NUMBER: US 60/099,136
SAFLIER PILLING DATE: 1998-09-04
SOFTWARE: Patentin Ver: 2.0
SEQ.ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      514 AYSQDTGLFYVP-ANHWKED------YWTEEVSYTKGSAYLG------
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                                                                                                                                                                                                                                                                                                                            16 APVOSVVF-AQTN----NSESPAPILRWSAEDKHNEGINSH----
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
| LENGTH: 685
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U8-09-390-234-14
'Sequence 14, Application US/09390234
'Perent No. 6365390
'GENERAL INFORMATION:
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                                                                                                                                                                        r TYPE: PRT condomonas aeruginosa US-09-252-991A-32033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 HLW 275
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Patent No. 6602700

| Patent No. 6602700
| GENERAL INFORMATION:
| APPLICANT: Li, Xin-Liang
| APPLICANT: Li, Xin-Liang
| APPLICANT: Li, Xin-Liang
| APPLICANT: Azain, Michael J.
| APPLICANT: Azain, Michael J.
| APPLICANT: Blum, David L.
| APPLICANT: Blum, David L.
| APPLICANT: Blum, David L.
| APPLICANT: Blum, David L.
| APPLICANT: Blum, David L.
| APPLICANT: Blum, David L.
| APPLICANT: Rataeva, Irina
| TITLE NETRENCE: 67-98
| TITLE REFERENCE: 67-98
| TITLE REFERENCE: 67-98
| TITLE APPLICATION NUMBER: US 60/099,136
| PRIOR APPLICATION NUMBER: US 60/099,136
| PRIOR APPLICATION NUMBER: US 60/099,136
| PRIOR APPLICATION NUMBER: US 60/099,136
| PRIOR APPLICATION NUMBER: US 60/099,136
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                  166 --AANFTNLSYPM-----GFHSKYENFVDTIKONYIVSDSNGYWNWKGANPEDWIEG 215
QSVVFAQTNNSESPAPILRWSAEDKHNEG---INSHLWIVNRAIDIMSRNTTIVNPNETA 75
                                                                                                                                                                                                                                                                                                                                                                                                         120 -----AKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLHYLGDVNQPMH----
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Patent No. 6602700
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                                                                                                                                                                                                                                                                                                              Gape
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1 Similarity 26.2%; Pred. No. 0.72;
44; Conservative 29; Mismatches 64; Indels 31;
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                    152 -LSLHYLGDVNQPMH-----AANFTNL---SYPMGFHSKYENFV---
                                                                                                                                                                                                                                                                              Query Match 6.1%; Score 93; DB 4; Length 275; Best Local Similarity 21.9%; Pred. No. 0.32; Matches 46; Conservative 31; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 13, Application US/09092315; Patent No. 6399337; GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Taylor, Diane E. APPLICANT: Ge, Zhongming; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE; FILER REFERENCE: 07254/04901; CURRENT APPLICATION NUMBER: US/09/092,315; CURRENT APPLICATION NUMBER: US 60/048,857; EARLIER APPLICATION NUMBER: US 60/048,857; EARLIER PILLING DATE: 1997-06-06; NUMBER OF SEQ ID NOS: 22; SOFTWARE: PRESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 DWFVKAAVSQEYADKWRAEVTPVTGKRLME 263
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ORGANISM: Helicobacter pylori
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Best Local Similarity
Matches 44; Conserva
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ORGANISM: Plant
         -09-510-322A-10
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Sequence 1, Application US/09733524A

Fatent No. 6534298
GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: US254-049002
CURRENT APPLICATION NUMBER: US 09/092,315
FRIOR PILLOR DATE: 1990-06-05
PRIOR FILLING DATE: 1990-06-06
PRIOR FILLING DATE: 1997-06-06
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                          173 SYPMGFHSKYENP---VDTIKNNYIVSDSNGYWNWKGANPEDWIEGAA 217
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173 SYPMGFHSKYENF --- VDTIKNNYIVSDSNGYWNWKGANPEDWIEGAA
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APPLICANT: TAYLOR, Diane B.
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001.
CURRENT APPLICATION NUMBER: US/09/092,315
CURRENT FILING DATE: 1998-06-05
EARLIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FABLESQ for Windows Version 3.0
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26.2%; Pred. No. 1;
tive 29; Mismatches 64;
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SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                      US-09-092-315-1
; Sequence 1, Application US/09092315
; Patent No. 6399337
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US-09-092-315-1
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ORGANISM: Helicobacter pylori
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Matches 44; Conservative
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Best Local Similarity
Matches 44; Conserv
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ORGANISM: Helicobacter pylori
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          ; UKGANISM: nc.
US-09-733-524A-7
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Sequence 7, Application US/09733524A

Patent No. 6534298

GENERAL INPORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming

TITLE OF INVENTION: WOLLEL CACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REFRENCE: 0724-049002

CURRENT APPLICATION NUMBER: US/09/733,524A

CURRENT FILING DATE: 2000-12-07

PRIOR APPLICATION NUMBER: US 69/092,315
PRIOR PLILING DATE: 1998-06-05

PRIOR PLILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 478

TYPE: PRI
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                         NPNETALLNEWRADLENGIYSADYENPYYDNSTYASHFYD-----PDTG-----TTYIP 118
                                                                             119 FAKHAKETGAKY-FNLA-----GQAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANFTNL 172
                                                                                                      119 FAKHAKETGAKY-FNLA-----GOAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANFTNL 172
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                                                                                                                                                                                   277 SF-VNVHD-FKNFDEAIDYIK--YLHTHKNAYLDMLYENPLNTLDGKA 320
                                                                                                                                                          SYPMGFHSKYENF --- VDTIKNNYIVSDSNGYWNWKGANPEDWIEGAA 217
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Petent No. 639937
Petent No. 639937
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Petent No. 639937
Petent No. 6399337
Petent Septicant Application NUMBER: US/09/092,315
CURRENT FILING DATE: 1999-06-05
PEALIER PETING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
POSTWARE FEALSE FEATSON NUMBER: US 60/048,857
PERILIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
PETENT PARTICAL NOS: 22
NOSTWARE FEATSON OF MINDOWS VERSION 3.0
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ORGANISM: Helicobacter pylori
US-09-092-315-7
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Best Local Similarity
Matches 44; Conserva
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RESULT 15
US-09-252-991A-17709
US-09-252-991A-17709
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Facence 17709, Application US/09252991A
FILE REPERRECE 107196.136
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR FILING DATE: 1999-02-18
FRIOR FILING DATE: US 60/074,788
FRIOR FILING DATE: US 60/094,190
FRIOR FILING DATE: US 60/094,190
FRIOR FILING DATE: US 60/094,190
FRIOR FILING DATE: US 60/094,190
FRIOR FILING DATE: US 60/094,190
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                                                                                                                                           70 NPNETALLINEWRADLENGIYSADYENPYYDNSTYASHFYD-----PDTG-----TTYIP 118
                                                                                                                                                                                                119 FAKHAKETGAKY-FNLA-----GQAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANFTNL 172
                                                                                                                                                                                                                                                                                                                                        357 KALLGYPEEKQAAIERVANRHTAVEKYQF-DWLRQLLRDGRPQPMLDAYADTRRDGAYPA 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 ---MGFHSKYENFVDTIKNNYIVSDSNGYWNW-----KGANPEDWIEGAAVAAKQD-YPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 NPNETALLNEWRADLENGIYSADYENPYYDNSTYASH---FYDPDTGTTY--IPFAKHA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 SYPMGFHSKYENP --- VDTIKNNYIVSDSNGYWNWKGANPEDWIEGAA 217
6.0%; Score 91.5; DB 4; Length 478; 26.2%; Pred. No. 1.1; ive 29; Mismatches 64; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.0%; Score 91.5; DB 4; Length 503; Best Local Similarity 20.3%; Pred. No. 1.1; Matches 42; Conservative 37; Mismatches 93; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 VVNDTTKDWFVKAAVSQEYADKWRAEV 253
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Job time : 19 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
                                  Best Local Similarity 26.28
Matches 44; Conservative
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; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
US-10-421-654-2
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ORGANISM: Unknown
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Sequence 16747, A
Sequence 4, Appli
Sequence 82, Appli
Sequence 90, Appl
Sequence 98, Appl
Sequence 32, Appl
Sequence 106, Appl
Sequence 106, Appl
Sequence 73670, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Appl
Sequence 2, Appli
Sequence 219446,
Sequence 17, Appl
                                                                                            July 27, 2004, 14:46:13; Search time 47 Seconds (Without alignments) 1878.925 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                       PCT-US03-12556-2
1522
1 MKKKVLALAAMVALAAPVQS:.......EAQRVTAGYIHLWFDTYVNR 282
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

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9: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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5 US-10-369-493-16747

5 US-10-421-654-4

5 US-10-421-654-82

5 US-10-421-654-82

5 US-10-421-654-90

5 US-10-421-654-90

5 US-10-421-654-106

5 US-10-421-654-106

6 US-10-421-654-106

70-10-282-122A-73670

105-09-858-525A-10

US-09-858-525A-10

US-09-858-525A-10

US-10-424-599-219446
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                Scoring table:
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Maximum DB e
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                                                                                                     Run on:
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Sequence 13, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 13784, A
Sequence 13784, A
Sequence 239478,
Sequence 239478,
Sequence 27717, Ap
Sequence 27717, Ap
Sequence 27718, Appli
Sequence 27, Appli
Sequence 2, Appli
Sequence 2, Appli
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2 US-10-282-122A-55192

3 US-10-067-385-6

2 US-10-424-599-264682

3 US-10-120-319-13

4 US-10-120-319-1

4 US-10-189-977-1

4 US-10-189-977-1

4 US-10-189-977-1

4 US-10-189-977-7

4 US-10-189-977-7

4 US-10-189-977-7

4 US-10-189-977-7

5 US-10-189-977-7

6 US-10-189-977-7

7 US-10-189-977-7

8 US-10-189-977-7

9 US-10-282-122A-4689

1 US-10-282-122A-70739

1 US-10-383-930-39

1 US-09-843-007-2

6 US-10-282-122A-70739

1 US-09-843-007-2

6 US-10-282-122A-71305

1 US-09-843-007-2

6 US-10-282-122A-1305

1 US-09-733-524-1

6 US-10-383-930-39

1 US-09-733-524-1

6 US-10-437-963-191038

2 US-10-282-122A-77188

6 US-10-437-963-191038

2 US-10-282-122A-77188

6 US-10-474-776-429

6 US-10-474-776-429
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ALIGNMENTS

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61 IMSRNTTIVNPNETALLNEWRADLENGIYSADYENPYYDNSTYASHFYDPDTGTTYIPFA 120
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Sequence 2, Application US/10421654

Publication No. US20040005604A1

GENERAL INFORMATION:

APPLICANT: Gramatikova, Svetlana
APPLICANT: Hazlewood, Geoff
APPLICANT: Lam, David E.

APPLICANT: Lam, David E.

APPLICANT: Barton, Nelson E.

TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM AND
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: WOMBER: US/10/421,654

CURRENT APPLICATION NUMBER: US/10/421,654

CURRENT FILING DATE: 2003-04-21

PRIOR FILING DATE: 2002-04-19

NUMBER OF SEQ ID NOS: 106

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKKVLALAAMVALAAPVQSVVFAQTINNSESPAPILRWSAEDKHNEGINSHLMIVNRAID
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100.0%; Score 1522; DB 15; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.9e-139;
Matches 282; Conservative 0; Mismatches 0; Indels 0;
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OTHER INFORMATION: Obtained from an environmental sample
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61 IMSRNTTIVNPNETALLINEWRADLENGIYSADYENPYYDNSTYASHFYDPDTGTTYIPFA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 KHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANFTNLSYPMGFHS 180
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Sequence 6, Application US/10421654

Publication No. US20040005604A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Haalewood, Geoff
APPLICANT: Haalewood, Geoff
APPLICANT: Ham, David E.
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 0910-094001
FILE REFERENCE: 0910-094001
CURRENT APPLICATION NUMBER: US 60/374,313
FRIOR FILING DATE: 2003-04-21
FRIOR FILING DATE: 2002-04-19
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSEQ for Windows Version 4.0
ILENGTH: 280
ILENGTH: 280
ILENGTH: 280
ILENGTH: REATURE:
CORRENTED FOR MINDOWING PERMINGS INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME INCOME IN
             APPLICANT: Carmatikova, Svetlana
APPLICANT: Hazlewood, Geoff
APPLICANT: Lam, David B.
APPLICANT: Lam, David B.
APPLICANT: Lam, David B.
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM AND TITLE OF INVENTION: WENTHODS FOR MAKING AND USING THEM FILE REPERENCE: 09010-094001
CURRENT APPLICATION NUMBER: US/10/421,654
CURRENT FILING DATE: 2003-04-21
PRIOR PILING DATE: 2003-04-21
PRIOR FILING DATE: 2002-04-19
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 80.9%; Score 1232; DB 15; Length Best Local Similarity 76.5%; Pred. No. 3e-111; Matches 215; Conservative 35; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Obtained from an environmental sample
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; LOCATION: (1)...(24)
US-10-421-654-4
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Foulication No. US20030233675A1

GENERAL INFORMATION:
FAPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Glater, Steven C.
APPLICANT: Glater, Steven C.
APPLICANT: Glater, Steven C.
APPLICANT: Gladman, Barry S.
APPLICANT: Gladman, Barry S.
APPLICANT: Gladman, Barry S.
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APPLICANT: Gladman, Barry S.
APPLICANT: Gladman, Barry S.
APPLICANT: Gladman, Barry S.
APPLICANT: ALIANG DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-28
NUMBER: OF SEQ ID NOS: 47374
SEQ ID NO 16747

APPLICANT: 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 SKYENFVDTIKDNYKVTDGNGYMNWKGTNPEDWIHGAAVVAKQDYAGIVNDNTKDWFVRA 240
121 KHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANFTNLSYPMGFHS 180
                                                                                                                                                                                                                                                                                                   181 KYENFVDTIKONYIVSDSNGYWNWKGANPEDWIEGAAVAAKQDYPGVVNDTIKDWFVKAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 AKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANFTNLSYPMGFH 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.6%; Score 1257.5; DB 15; Length 397; 80.2%; Pred. No. 1.6e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVSQEYADKWRAEVTPMTGKRLMDAQRVTAGYIQLWFDTYGNR 283
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                                                                                                                                                                                                                                                                                                                                                                         241 VSQEYADKWRAEVTPVTGKRLMEAQRVTAGYIHLWFDTYVNR 282
                                                                                                                                                                                                                                                                                                                                                                                                               241 VSOEYADKWRAEVTPVTGKRLMEAORVTAGYIHLWFDTYVNR 282
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NAME/KEY: unsure
LOCATION: (1)..(397)
OTHER INFORMATION: unsure at all Xaa locations
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; Sequence 4, Application US/10421654
; Publication No. US20040005604A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 80.2%
Matches 227; Conservative
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                                                                    LGLSLHYLGDVNQPMHAANFTNL-SYPMGFHSKYENFVDTIKNNYIVSDSNGYWNWKGAN 208
                                                                                                    209 -PEDWIEGAAVAAKQDYPGVVNDTTKDWFVKAAVSQEYADKWRAEVTPVTGKRLMEAQRV 267
                                                                                                                                                                                         50 SHLWIVNRAIDIMSRN-TTIVNPNETALLN--EWRADLENGIYSADYENPYYDNST---- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 -----YASHFYDPDTGTTYIPFAKHAKE----TGAKYFNLAGQAYQNQDMQQAFFY 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 IDGLIKGGWKSHPYDPDTRKNY----KGEBEPTALSOGDKYPKLAGDYFKKEDWKQAFYY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGLSLHYLGDVNQPMHAANFTNL-SYPMGFHSKYENFVDTIKNNYIVSDSNGYWNWKGAN 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 - PEDWIEGAAVAAKODYPGVVNDTTKDWFVKAAVSOEYADKWRAEVTPVTGKRLMEAORV 267
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 90, Application US/10421654
; Sequence 90, US20040005604A1
; GRERRAL INFORMATION:
    APPLICANT: Gramatikova, Svetlana
    APPLICANT: Hazlewcod, Geoff
    APPLICANT: Lam, David E.
    APPLICANT: Lam, David E.
    APPLICANT: BARTON, NETHONE FOR MAKING AND USING THEM
    TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
    TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
    TITLE OF INVENTION: WHERE: US/10/421,654
    CURRENT FILING DATE: 2003-04-21
    FRIOR APPLICATION NUMBER: US 60/374,313
    PRIOR APPLICATION NUMBER: US 60/374,313
    PRIOR FILING DATE: 2002-04-19
    NUMBER OF SEQ ID NOS: 106
    SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.8%; Score 515; DB 15; Length 47: 38.7%; Pred. No. 3.2e-41; Artive 42; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: Obtained from an environmental sample
                                                                                                                                                                                                                                                           TAGYIHLWFDTYV 280
                                                                                                                                                                                                                                                                                    |||:||||| |:|
290 TAGFIHLWFKTFV 302
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TAGFIHLWFKTFV 302
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US-10-421-654-90
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Best Local Similarity
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ORGANISM: Unknown
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                                                                                                                                                                                                                                                                                                                                                                            DIMSONTTVVKONETALLNEWRINLEEGIYSADYKNPYYDNSTFASHFYDPDSEKTYIPF 116
                                                                                                                                                                                                                                                                                                                                                                                                                             AKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANFTNLSYPMGFH 179
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Sequence 82, Application US/10421654

Sequence 82, Application US/10421654

Publication No. US20040005604A1

GENERAL INFORMATION:
APPLICANT: Gramatikova, Svetlana
APPLICANT: Hazlewood, Geoff
APPLICANT: Barton, Nelson R.
TITLE OF INVENTION: PROSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM AND
TITLE OF INVENTION: PROSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM AND
FILE REFERENCE: 09010-094001

CURRENT FILING DATE: 2003-04-21

PRIOR PILING DATE: 2003-04-21

PRIOR PILING DATE: 2002-04-19
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                                                                                                                                                                                                                                                              1 MKRKILAIASVIALTAPIOSVAFAH----ESDGPIALRWSAESVHNEGVSSHLWIVNRAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKYENFVDTIKNNYIVSDSNGYMNWKGANPEDWIEGAAVAAKQDYPGVVNDTTKDWFVKA
                                                                                                                                        Query Match 79.3%; Score 1206.5; DB 15; Length 280; Best Local Similarity 76.2%; Pred. No. 8.9e-109; Matches 215; Conservative 34; Mismatches 28; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.3%; Score 522; DB 15; Length 473; 38.7%; Pred. No. 6.7e-42; ive 43; Mismatches 105; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 AVSQDSADKWRAEVTPVTGKRLMEAQRITAGYIHLWFDTYVN 278
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    OTHER INFORMATION: Obtained from an environmental sample
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 82
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Best Local Similarity 38.77
Matches 121; Conservative
                                            ; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
US-10-421-654-6
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; LOCATION: (1)...(25)
US-10-421-654-82
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ORGANISM: Unknown
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; LOCATION: (1)...(30)
US-10-421-654-106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 IDGLIRGGWKSHFYDPDTRKNY----KGEEFTALSQGDKYFKLAGEYFKKNDWKQAFYY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 SHIMIVNRAIDIMSRN-TTIVNPNETALLN--EWRADLENGIYSADYENPYYDNST---- 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKRKLCTWALVTALASSTAVIPTAARACGLGEVIKQENQEHK--RVKRWSAEHPHHSHES 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKKVLALAAMVALAAPVQSV-----VFAQTNNSESPAPILRWSAEDKHNEGIN 49
Sequence 98, Application US/10421654
Publication No. US20040005604A1
Publication No. US20040005604A1
GENERAL INFORMATION:
APPLICANT: GARMATION:
APPLICANT: Hazlewood, Geoff
APPLICANT: Lam. David E.
APPLICANT: Lam. David E.
APPLICANT: Lam. David E.
APPLICANT: David E.
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM APPLICANT: ON PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM FILE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM APPLICANTON: PHOSPHOLIPASES, NUCLEIC ACIDS ENCOPING THEM FILE OF INVENTION: PHOSPHOLIPASE: US/10/421,654
CURRENT APPLICATION NUMBER: US 60/374,313
PRIOR APPLICATION NUMBER: US 60/374,313
PRIOR APPLICATION NUMBER: US 60/374,313
PRIOR APPLICATION NUMBER: US 60/374,313
PRIOR APPLICATION NUMBER: US 60/374,313
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PRIOR APPLICATION UMBER: US 60/374,313
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Publication No. US20040005604A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Gramatikova, Svetlana
APPLICANT: Hazlewood, Geoff
APPLICANT: Lam, David E.
APPLICANT: Lam, David E.
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM AND
TITLE OF INVENTION: PRESPHOLIPASES, NUCLEIC ACIDS ENCODING THEM AND
TITLE OF INVENTION: PRETHODS FOR MAKING AND USING THEM
FILLE REFERENCE: 09010-09401.
CURRENT APPLICATION NUMBER: US/10/421,654
CURRENT FILING DATE: 2003-04-21
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33.4%; Score 509; DB 15; Length 473;
Best Local Similarity 37.8%; Pred. No. 1.2e-40;
Matches 119; Conservative 43; Mismatches 109; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Obtained from an environmental sample
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| NAME/KEY: SIGNAL
| LOCATION: (1)...(25)
| US-10-421-654-98
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50 SHLWIVNRAIDIMSRN-TTIVNPNETALLN--EWRADLENGIYSADYENPYYDNST---- 102
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| Publication No. US20040005604A1
| GENERAL INFORMATION:
| APPLICANT: Gramatikova, Svetlana |
| APPLICANT: Hazlewood, Geoff |
| APPLICANT: Lam. David E. |
| APPLICANT: Lam. David E. |
| APPLICANT: Lam. David E. |
| APPLICANT: Barton, Nollson R. |
| TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM AND |
| TITLE OF INVENTION: PRETHOUS FOR MAKING AND USING THEM AND |
| FILE REFERENCE: 09010-094001 |
| CURRENT APPLICATION NUMBER: US/10/421,654 |
| CURRENT FILING DATE: 2003-04-21 |
| PRIOR APPLICATION NUMBER: US 60/374,313 |
| PRIOR APPLICATION NUMBER: US 60/374,313 |
| PRIOR APPLICATION NUMBER: US 60/374,313 |
| PRIOR APPLICATION NUMBER: US 60/374,313 |
| PRIOR APPLICATION NUMBER: US 60/374,313 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 -----YASHFYDPDTGTTYIPPAKHAKE----TGAKYFNLAGQAYQNQDMQQAFFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.9%; Score 501; DB 15; Length 47
36.5%; Pred. No. 7.4e-40;
tive 49; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Obtained from an environmental sample
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PRIOR APPLICATION NUMBER: US 60/374,313
PRIOR FILING DATE: 2002-04-19
NUMBER OF SEQ ID NOS: 106
SEQ ID NO 32
LENGTH: 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 36.5% Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-421-654-32
                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Unknown
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US-10-282-122A-73670

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12;
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                                                                                                                                                                                                                                                                                                                                  120 AKHAKE---TGAKYFNLAG----QAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANFT 170
                                                                                                                                                                                                                                                                                                                                                                                   DAKRREHRGTNAGTDDIAGWWAESLQAYRAGAKERAYFVLGVVLHMVEDMGVPAHA---- 146
                                                                                                                                                                                                                                                                                                                                                                                                                                          171 NLSYPMGFHSKYENFVDTIKNNYIVSDSNGYWNWKG-------ANPEDWIEGAAV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 NGVYHQGNLTEFDNF------EFMGLSNWKPSFADINRTDPGYADPSRYYEFSRD 195
                                                                                                                                          1 MKKKVLALAAMVALAAPVQSVVFAQTNNSESPAPILRWSAEDKHNEGINSHLMIVNRAID 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 AAKQDYPGV--VNDTTKDWFVKAAVSQEYADKWRAEVTPVTGKRLMEAQRVTAG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - See File Wrapper or PALM
7.9%; Score 120; DB 15; Length 251;
Larity 20.4%; Pred. No. 0.0035;
Conservative 48; Mismatches 108; Indels 7
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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Remaining Prior Application data removed
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PRIOR FILING DATE: 2000-03-21
PRIOR PRICATION NUMBER: 60/191, 078
PRIOR PELICATION NUMBER: 60/206, 848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-66
PRIOR PELICATION NUMBER: 60/230, 335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/245, 578
PRIOR APPLICATION NUMBER: 60/253, 879
PRIOR PILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
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EQ ID NO 73670
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Yamamoto, Robert
Forsyth, R.
Xu, H.
                    l Similarity
60; Conserv
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Query Match
Best Local S
Matches 60
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Expansion David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: CAN TOWN THUA
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(3323) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                            61 SQDFKEKKTAVIKEKEVVSKNPVIDNNTSNEEAKIKEENSNKSQGDYTDSFVNKNTENPK 120
                                                                                                                                                                                                                               97 YYDNSTYASHFYDPDTGTTYIPFAKHAKETGAKY----FNLAGQAYQ----NQD---- 142
                                                                                                                                                                                                                                                     121 KEDKVVYIAEFKDKESGEKAIKELSSLKNTKVLYTYDRIFN--GSAIETTPDNLDKIKQI 178
                                                                                                                                                                                                                                                                                                         143 ------TNLSYPMGF 178
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                                                                                                  QTINNSESPAPILRWSAEDKHNEGINSHLWIVNRAIDIMSRNTTIVNPNETALLNEWRADL
                                                                            1 MKKKV---LALAAMVALAAPVQSVVFAQTNNSESPAPI--LRWSAEDKH-NEGINSHL--
                                      Gaps
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                                      66
  Length 2140;
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                                    39; Mismatches 109; Indels
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US-10-424-599-239481
  DB 12;
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Score 108.5; Di
Pred. No. 0.88;
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; Sequence 239481,
Publication No. US20040031072A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 KQDY-----PGVV--NDTTKD 234
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Query Match 7.1%;
Best Local Similarity 23.8%;
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Best Local Similarity 21.8*
Matches 51; Conservative
                                    77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
6.3%; Score 96.5; DB 9; Length 8
Best Local Similarity 21.0%; Pred. No. 3.5;
Matches 64; Conservative 48; Mismatches 140; Indels
                                                                   APPLICANT: BOETS, Annemie
APPLICANT: BOETS, Annemie
APPLICANT: BOETS, Annemie
APPLICANT: ANN RIE, Jercen
APPLICANT: DAMME, Nicola
TITLE OF INVENTION: No. US20020199215A1e1 Toxins
FILE REFERENCE: 021565-07
CURRENT FILING DATE: 2001-05-17
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PRECEIN VERSION 3.0
SOFTWARE: 936
IENGTH: 936
TYPE: PRI
TYPE: PRI
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APPLICANT: BOETS, Annemie
APPLICANT: ARNAUT, Greta
APPLICANT: DANN RIE. Jeroen
APPLICANT: DANNE, Nicole
TITLE OF INVENTION: No. US20020199215A1e1 Toxins
FILE REFERENCE: 021565-07
CURRENT APPLICATION NUMBER: US/09/858,525A
CURRENT FILING DATE: 2001-05-17
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
                      Sequence 10, Application US/09858525A Publication No. US20020199215A1 GENERAL INFORMATION:
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# Publication No. US20020199215A1
# GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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US-09-858-525A-10
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Sequence 219446, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Avoalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 211446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 SRNTTIVNPNETALLNEWRADLENGIYSADYENPY-----YDN-STYASHFYDPDŢ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 NLSYPMGFHSKYENFVDTIKNNYIVSDSNG----YWNWKGANPEDWIEGAAV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                            DB 9; Length 871;
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                                                                                                                                                                                                                                                                                                                                          Query Match
6.3%; Score 96.5; DB 9; Length 8
Best Local Similarity 21.0%; Pred. No. 3.7;
Matches 64; Conservative 48; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 ASHFYD-PDTGTTYIPFAKHAKETGAKYFNLAGQA----YQNQ--
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US-10-424-599-219446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)..(293)
OTHER INFORMATION: unsure at all Xaa locations
; SEQ ID NO 2
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Brevibacillus laterosporus
US-09-858-525A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 WPDTY 279
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582 YVDEY 586
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Sequence 17, Application US/09733524

Fatent No. US20020068347A1

GENERAL INFORMATION:

APPLICANT: The Governers of the University of Alberta, a Canada Corporation

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: To a Canada Corporation

TITLE OF INVENTION: WUCLEIC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: EXPRESSING THEM

FILLE REFERENCE: 0724/049002

CURRENT APPLICATION NUMBER: US/09/733,524

CURRENT FILING DATE: 1998-06-05

FRIOR APPLICATION NUMBER: 60/048,857

FRIOR FILING DATE: 1998-06-06

SPRIOR FILING DATE: 1998-06-06

SOFTWARE: FastsEQ for Windows Version 4.0

SEQUENCE: And ADDIA TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAYLOR TO TAY
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Best Local Similarity 26.2%; Pred. No. 3.2;
Matches 44; Conservative 29; Mismatches 64; Indels 31; Gaps 10;
                                                 70 NPNETALLNEWRADLENGIYSADYENPYYDNSTYASHFYD-----PDTG----TTYIP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 NVKNKNEFTSQYKFNLCFENTQGYGYVTEKIIDAYFSHTIPIYW----GSPSVAKDFNPK 277
178 FHSKYENFVDTIKNNYIVSDSNGYWNWKGANPEDWIEGAAVAAKQDYPGVVNDTTKDWFV 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 FAKHAKETGAKY-FNLA----GQAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANFTNL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYPMGFHSKYENF---VDTIKNNYIVSDSNGYWNWKGANPEDWIEGAA 217
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                                                                                                                                                                                                                                                  238 KAAVSQEYADKWRAEVTPVTGKRLMEAQRVTAGYIHLWPDT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT .
ORGANISM: Helicobacter pylori fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: PEPTIDE
; LOCATION: (0) ...(0)
; OTHER INFORMATION: Strain 763 from NCTC11639
US-09-733-524-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173
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Search completed: July 27, 2004, 14:49:15 Job time : 48 secs Colosu) MIDIA OCO SILI

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 27, 2004, 14:38:52; Search time 17 Seconds (without alignments) 1595.648 Million cell updates/sec

PCT-US03-12556-2 1522 1 MKKKVLALAAAWVALAAPVQS........EAQRVTAGYIHLWFDTYVNR 282 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	& Query Match	% Query Match Length	DB	SUMMARIES ID	Description
1	1252.5	82.3	592	~	PS0197	phospholipase C (E
~	511.5	33.6	289	7	C43868	lecithinase - List
۳	511	33.6	289	7	AF1100	phospholipase C [i
4	509	33.4	289	7	S20888	phospholipase C (E
'n	314.5	20.7	178	7	T43165	Q
9	254	16.7	398	7	B30565	phospholipase C (E
7	231	15.2	398	~	JQ0366	phospholipase C (E
œ	229	15.0	398	7	A30565	phospholipase C (E
6	227	14.9	398	7	B49231	phospholipase C, a
0	0	7.2	245	~	H97025	phospholipase C re
٦.	108.5	7.1	2140	N	F95074	serine proteinase,
7	107	7.0	2144	~	A97942	metalloproteinase
'n	103	6.9	625	7	G97076	alkaline phosphata
4.	102.5	6.7	470	7	AF1972	hypothetical prote
Ŋ	102	6.7	562	7	855516	glucan 1,3-beta-gl
ب	102	6.7	2358	7	T39569	probable alpha-glu
۲.	66	6.5	273	~	D82862	conjugal transfer
æ	98	6.4	472	~	E98020	hypothetical prote
6	97.5	6.4	363	~	AE0616	outer membrane pro
20	97	6.4	468	~	H64802	
Ξ.	97	6.4	653	~	F85620	partial fimbrial u
2	97	6.4	653	~	H90756	partial fimbrial u
e		6.3	532	~	D96966	beta-mannanase Man
24	95.5	6.3	418	٦	A53888	thermolabile hemol
25		6.3	1283	7	S52500	oxysterol-binding
9		6.2	441	~	E90051	hypothetical prote
	95	6.2	624	~	E64483	hypothetical prote
28	95	6.2	1599	~	S22737	glucosyltransferas
6	94.5	6.2	305	~	H86245	bifunctional nucle

quinoprotein alcoh endo-1,4-beta-xyla	fimbrial adhesin F methyl-accepting c	inner membrane pro	seed storage prote	hypothetical prote	dnaJ homolog prote	hypothetical prote	hypothetical prote	outer membrane por	hypothetical prote	cytosol nonspecifi	chitinase - Strept	hypothetical prote
B83399 A31842	S04072 F82383	G81692	S24263	H87347	873361	A82940	AE2218	843159	G83212	JC6042	T35345	A87389
7	7	01 17	4 (7	~	н	~	7	7	~	н	7	N
623 837	277	787	304	538	910	782	358	363	441	474	296	342
6.6	6.1	6.1	. 1.9	6.1	6.1	0.9	0.9	0.9	9	9	6.0	6.0
9 4 4 4	93.5 93.5	93.5	92.5	92.5	92.5	92	91.5	91.5	91.5	91.5	91	91
30	332	34	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 PS0197 Phospholipase C (EC 3.1.4.3) precursor - Bacillus cereus
N;Alternate names: cereolysin AB; phosphatidylcholine-hydrolyzing phospholipase C C:Species: Bacillus cereus
C;Date: 30-Sep-1991 #sequence_revision 26-Apr-1996 #text_change 15-Oct-1999
C; Accession: \$18978; PS0197; I40160; S01949; A32042; S03200; I40161
R; Kuzmin, N.P.; Gavrilenko, I.V.; Krukov, V.M.; Karpov, A.V.
submitted to the EMBL Data Library, January 1992
A; Description: Fused genes phospholipase C and sphingomyelinase Bacillus cereus ensuring
A; Reference number: S18978
A;Accession: S18978
A;Status: preliminary
A; Molecule type: DNA
A;Residues: 1-592 <kuz></kuz>
A; Cross-references: EMBL: X64140; NID: 939421; PIDN: CAA45501.1; PID: 939422
R;Ikeda, K.; Inoue, S.; Amasaki, C.; Teshima, K.; Ikezawa, H.

J. Biochem. 110, 88-95, 1991 Ayfitle: Kinetices of the hydrolysis of monodispersed and micellar phosphatidylcholines c A;Reference number: PS0197; MUID:92041771; PMID:1939031 A;Accession: PS0197

A;Molecule type: protein A;Residues: 39-49 <IKE> R;Gavrilenko, I.V.; Baida, G.E.; Karpov, A.V.; Kuz'min, N.P. Bioorg. Khim. 19, 133-138, 1933 A;Title: [Nuclectide sequence of phospholipase C and sphingomyelinase genes from Bacillu A;Reference number: 140160; MUID:93249510; PMID:8387306

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1-592 <RES.
A;Cross-recences: EMBL:X64140; NID:g39421; PIDN:CAA45501.1; PID:g39422; EMBL:X64141; N
R;Johansen, T: Haugli, F.B.; Ikezawa, H.; Little, C.
Nucleic Acids Res. 16, 10370, 1988
A;Title: Bacillus cereus strain SE-1: nucleotide sequence of the sphingomyelinase C gene
A;Reference number: S01949; MUID:89057484; PMID:2848222
A;Accession: S01949

A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA

A; Residues: 1-283 <10H>
A; Residues: 1-283 <10H>
A; Cross-references: BMBL:X12854; NID:939444; PIDN:CAA31332.1; PID:9295765
A; Accossion: 4. Cross-references: BMBL:X12854; NID:939444; PIDN:CAA31332.1; PID:9295765
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1988
R; Gilmore, M.S.; Cruz-Rodz, A.L.; Leimeister-Waechter, M.; Kreft, J.; Goebel, W.
J. Bacteriol. 171, 744-753, 1989
A; Title: A Bacillus cereus cytolytic determinant, cereolysin AB, which comprises the pho A; Reference number: A32042; MUID:89123149; PMID:2536680

A;Status: preliminary

A,Molecule type: DNA*
Mresidues: 1-8,70',10-13,'L',15-30,'QRFGVIP',38-76,'L',78-119,'Y',121-211,'D',213-225,'
A;Residues: 1-8,70',10-13,'L',15-30,'QRFGVIP',38-76,'L',78-119,'Y',121-211,'D',213-225,'
A;Cross-references: GB:M24149; NID:g142672; PIDN:AAA91819.1; PID:g142673
R;Yamađa, A.; Tsukagoshi, N.; Udaka, S.; Sasaki, T.; Makino, S.; Nakamura, S.; Little, C.

```
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Date: 27-Nov-2001
R;Glaser, D: 7: Bachrieser, C:; Buchaud, B:; Durand, L:; Dussurget, O:; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A;Authors: Kreft, J:; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, B.; Maitournam, A.; Ma
A;Authors: Kreft, J:; Kuhn, M.; Tisteria, Species.
A;Reference number: AB1077; MUID:21837279; PMID:11679669
A;Accession: A:100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phospholipase C (EC 3.1.4.3) precursor - Listeria monocytogenes (fragment)
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 16.58p-1992 #sequence_revision 16.58p-1992 #text_change 24.58p-1999
C;Accession: $20888
R;Domann, E.; Wehland, U.; Rohde, M.; Pistor, S.; Hartl, M.; Goebel, W.; Leimeister-Waec
R;Domann, E.; Wehland, U.; Rohde, M.; Pistor, S.; Hartl, M.; Goebel, W.; Leimeister-Waec
A;Title: A novel bacterial virulence gene in Listeria monocytogenes required for host ce
A;Reference number: $20887; MUID:92258410; PMID:1582425
A;Accession: $20888
A;Accession: $20888
A;Accession: $20888
A;Residues: 1-289 <a href="https://doi.org/10.100/19.2004">https://doi.org/10.100/19.2004</a>
A;Cross-references: EMBL:X59723; NID:g44091; PIDN:CAA42408.1; PID:g44093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-289 <LLA
A;Exseidues: 1-289 <LLA
A;Experimental source: strain EGD-e
                                                  SHLWIVNRAIDIMSRNTTIVNPNETALLNEWRADLENGIYSADYENPYYDNSTYASHFYD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 TNLSYPMGFHSKYENFVDTIKNNYIVSDSNGYMNWKGANPEDWIEGAAVAAKQDYPGVVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 NWKGANPEDWIEGAAVAAKODYPGVVNDTIKDWFVKAAVSQEYADKWRAEVTPVTGKRLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 PDTGTTYIPFAKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLHYLGDVNQPMHAANF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KKKVLALAAMVA-LAAPVQSVV-----FAQT----NNSESPAP-ILRWSAEDKHNEGIN
                                                                                                                                                                                                                                                                              phospholipase C [imported] - Listeria monocytogenes (strain EGD-e)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 DITKDWFVKAAVSQBYADKWRAEVTPVTGKRLMEAQRVTAGYIHLW 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 AKTKKSYLVG-----NSEWKKDTVEPTGARLRDSQQTLAGFLEFW 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.6%; Score 511; DB 2; Length 289; Best Local Similarity 37.1%; Pred. No. 5e-33; Matches 106; Conservative 55; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: plcB
C;Superfamily: Bacillus cereus phospholipase C
                                                                                                                                                271 DSQQTLAGFLEFW 283
                                                                                                                      EAQRUTAGYIHLW 275
                                                                                                                      263
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                            for
Bur. J. Blochem. 175, 213-220, 1988

A,Title: Nucleotide sequence and expression in Escherichia coli of the gene coding: A,Reference number: $01130; MUID:88296483; PMID:2841128
A,Recession: $03200
A,Molecule type: DNA
A,Residues: 166-211, 'D', 213-225,'A', 227-238,'R', 240-281,'N', 283 <YAM>A,Cross-references: EMBL:X12711; NID:g39439; PIDN:CAA31213.1; PID:g757735
C,Genetics: A,Gene: cerkB, plc
C,Reywords: phosphoric diester hydrolase
P,1-24/Domain: stopperide #status predicted <SIG>PID:A/ADDMAIN: propeptide #status predicted <SIG>PID:A/ADDMAIN: propeptide #status predicted <PRO>P;39-283/Product: phospholipase C #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIMSRNITIIVNPNBTALLNEWRADLENGIYSADYENPYYDNSTYASHFYDPDTGTTYIPF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKYENFVDTIKNNYIVSDSNGYMWKGANPEDWIEGAAVAAKQDYPGVVNDTIKDWFVKA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 SKYENFVDTIKDNYKVTDGNGYMNWKGTNPESWIHGAAVVAKQDYSGIVNDNTKDWFVKA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 DLENGIYSADYENPYYDNSTYASHFYDPDTGTTYIPFAKHAKETGAKYFNLAGQAYQNQD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 QIAQGIYDADHKNPYYDTSTFLSHFYNPDRDNTYLPGFANAKITGAKYFNQSVTDYREGK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 ARPHDIDSKLPHKLSMSADNPTNTDVNTHYWLFKQAEKILAKDVNHMRANLMNELKKFDK 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AKQAKETGAKYFKLAGESYKNKDMKQAFFYLGLSLHYLGDVNQPWHAANFTNLSYPQGFH
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKKKVLALAAMVALAAPVQSVVFAQTNNSESPAPIL-RWSAEDKHNEGINSHLWIVNRAI
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82.3%; Score 1252.5; DB 2; Length

Best Local Similarity 80.2%; Pred. No. 3.2e-91;

Matches 227; Conservative 23; Mismatches 32; Indels
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33.6%; Score 511.5; DB 2;
Best Local Similarity 38.7%; Pred. No. 4.5e-33;
Matches 98; Conservative 52; Mismatches 96;
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49 63 123 169 183 229 243

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A; Molecule type: DNA
A; Residues: 1-398 <SAI>
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T43165
probable phospholipase C (EC 3.1.4.3) - Listeria ivanovii (fragment)
N;Alternate names: lecithinase
C;Species: Listeria ivanovii
C;Species: ll.san-2000 #sequence_revision 11-Jan-2000 #text_change 02-Sep-2000
C;Accession: T43165
R;Gouin, E.; Dehoux, P.; Mengaud, J.; Kocks, C.; Cossart, P.
Infect. Immun. 63, 2739-2737, 1995
A;Title: LactA of Listeria ivanovii, although distantly related to Listeria monocytogene
A;Reference number: Z22322; MUID:95310034; PMID:7790091
A;Reference number: Z2332; MUID:95310034; PMID:7790091
A;Readues: L-178 cGOU3
A;Readues: L-178 cGOU3
A;Readues: L-178 cGOU3
A;Readues: L-178 cGOU3
A;Readues: L-178 cGOU3
A;Good C;Gonetics:
C;Genetics:
A;Gone: plob
C;Superfamily: Bacillus cereus phospholipase C
C;Keywords: phosphoric diester hydrolase
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                                                                                                                                                                                                                                  YLGDVNQPMHAANFTNLSYPMGFHSKYENFVDTIKNNYIVSDSNGYWNWKGANPEDWIEG 215
                                                                                                                                                                                                                                                                                                                                                                                        MSRNTTIVNPNETALLNEWRADLENGIYSADYENPYYDNSTYASHFYDPDTGTTYIPFAK 121
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phospholipase C (EC 3.1.4.3) precursor - Clostridium bifermentans C;Spocies: Clostridium bifermentans C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 23-Jun-1993 C;Accession: B30565
                                                                                                                                                                                                                                                                                                                                                                                                                                         216 AAVAAKQDYPGVVNDTTKDWFVKAAVSQBYADKWRAEVTPVTGKRLMEAQRVTAGYIHLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 NAKRAKADYPKIVNAKTKKSYLVG-----NSEWKKDTVEPTGARLRDSQQTLAGFLEFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 LRWSAEDKHNEGINSHLWIVNRAIDIMSRNTTIVNPNETALLNEWRADLENGIYSADYEN
                                                                                                                                                                                                                                                                                     PYYDNSTYASHFYDPDTGTTYIPFAKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLH
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                                                                                                                                                                         Gaps
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                                                                                                                                   Length 289;
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                                                                                                                                                                         92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
C;Genetics:
A;Gene: plcB
A;Gene: plcB
C;Superfamily: Bacillus cereus phospholipase C
C;Keywords: phosphoric diester hydrolase
C;Keywords: phosphoric diester hydrolase
F;1-25/Domain: signal sequence #status predicted <SIG>F;26-289/Product: phospholipase C #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                   33.4%; Score 509; DB 2; 39.6%; Pred. No. 7.2e-33;
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                                                                                                                                                                         47; Mismatches
                                                                                                                               Query Match
Best Local Similarity 39.64
Matches 95; Conservative
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gene from Clostridium perfringens
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N.Alternate names: Clostridium oedematiens beta- and gamma-toxins; Clostridium welchii (Species: Clostridium perfringens C;Species: Clostridium perfringens C;Species: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 15-Oct-1999
C;Accession: JQ0366
R;Saint-Joanis, B.; Garnier, T.; Cole, S.T.
Mol. Gen. Genet. 219, 453-460, 1989
A;Title: Gene cloning shows the alpha-toxin of Clostridium perfringens to contain both A;Reference number: JQ0366; MUID:90158507; PMID:2560137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 NGYWNWKGANP-----EDWIEGAAVAAKQDYPGVVNDTTKDWFVKAAVSQEYADKWRA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----KDLYYSHSTMSHSWDDW-- 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 QGVSILLENDMSKNEPESVRKNLEILKDNMHELQLGSTYPDYDKNAYD--LYQDHFWDPDT 102
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                                                                                                                                                                                                                                                                                                                                                                                                                54;
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Infect. Immun. 57, 468-476, 1989
A;Title: Cloning and expression of the phospholipase C gene from A;Reference number: A30565; MUID:89108588; PMID:2536356
A;Accession: B30565
A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-398 4750>
C;Keywords: phosphoric diester hydrolase
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                                                                                                                                                                                                                                                                                                                                       Query Match
16.7%; Score 254; DB 2; L.
Best Local Similarity 26.9%; Pred. No. 1.5e-12;
Matches 73; Conservative 49; Mismatches 95;
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Qy 113 GTTYIPFAKHAKETGAKYFNLAGQAYQNQDMQQAFFYLGLSLHYLGDVNQP 163 Db 103 DNNFSKDNSWYLAYSIPDTGRSQIKFSALARYENGRGNYKQATFYLGLSHHYLGDVNTP 162 Qy 164 MHAANFTALSYPMQFHSKYENFVDTIKNNYIVDSNGYWNWKGAN 208	RESULT 9 B492D1 B492D1 B492D2 B492D2 Copecies Clostridium perfringens Cipecies Clostridium perfringens Ristrevama, S.; Matesabita, O.; Minami, J.; Mizobuchi, S.; Okabe, A. Anticeria Land Company Anticeria Company Anti
Db 103 NNNFSKDNSWYLAYSIPDTGESQIRKFSALARYEWQRGNYKQATFYLGEAMHYFGDIDTP 162 Qy 164 MHAANFTNLSYPMGFHSKYENFVDTIKNNYIVSDSNGYMNWKGANPEDWIEGAAVAAKQD 223 Db 163 YHPANVTAVDSAGHVKFETFAEERKEQYKINTVGCKTNEDFYADILKNKD 212 Qy 224 YPGVVNDTTKDWFVKAAVSQEYADKWRAEVTFVTGKRLMEAQRVTAG 270 Db 213 FNAWSKEYARGFAKTGKSIYYSHASMSHSWDWDYAAKVTLANSQKGTAG 262 Qy 271 XIH 273 Db 263 XIY 265	Magacas Managas

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alkaline phosphatase superfamily protein [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C; Accession: G97076
R;Nolling, J:; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
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                      -- TNLSYPMGF 178
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A;Cross-references: GB:AE007317; PIDN:AAK99365.1; PID:g15458138; GSPDB:GN00174
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238 TGTDYRHKAMRIDDDAKASMRFKKEDLKGTDRAYWLSDKIPHAFNYYNGGKITVEKYDDG 297
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                                                                                                                                                             179 HSKYENFVDTIK------NNYIVSD----SNGYWNWKGANPEDWIEGAAVAA
                                                               EGISSVERAQKVQPMMNHARKEIGVEEAIDYLKSINAPF-GKNFDGRGMVISNIDTGTDY
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                      MOOAFFYLGL--SLHYLGDVNOPMHAANF---
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Matches 76; Conservative
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A;Status: preliminary
A;Molecule type: DNA
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A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97025
A;Accession: H97025
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-245 < KUR>
A;Experimental: A;Corsimental source: Clostridium acetobutylicum ATCC824
C;Genetics: A;Genetics: A;Geneti
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20.2%; Pred. No. 0.22;
ive 50; Mismatches 111;
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DNTRDYIRKNAKVANKIY-
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Best Local Similarity 20.2%;
Matches 51; Conservative
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C. Species of sp. PCC 7120

C. Species of sp. PCC 7120

A.Note: Note: Note of sp. PCC 7120

A.Note: Note: Note of sp. PCC 7120

C. Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C. Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C. Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C. Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C. Date: 14-Dec-2001 #sequence of the Virite; T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Datile: Complete Genomic Sequence of the Pilamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MulD:21595285; PMID:11759840

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-470 <KUR>
A.Residues: 1-470 <KUR>
A.Cross-references: GB:BA000019; PIDN:BAB73286.1; PID:g17130676; GSPDB:GN00179

A.Stperimental source: strain PCC 7120

C.Genetics:
A.Gene: alx1329
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A/Reference number: A96900; MUD:21359325, PMID:21359325
A/Accession: G97076
A/Status: prelimary
A/Status: prelimary
A/Residues: 1-625 <KUR>
A/Residues: 1-625 <KUR>
A/Residues: 1-625 <KUR>
A/Residues: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Genetics:
A/Genetics:
A/Genetics:
A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Genetics: A/Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 GAKYFNLAGQAYQNQDMQQAFFY--------LGLSLHYLGDVNQPMHAA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 ---NYTAVLHGYKEGFWNRNVMYKAEKPKDFFGEKSFNINENVGLGLSDKSFLNQ---- 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 MVALAAPVQSVVFAQTNNSESPAPILRWSAEDKHNBGINSHLWIVNRAIDIMSRNTTIVN 70
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22.0%; Pred. No. 1.8;
tive 51; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
6.8%; Score 103; DB
Best Local Similarity 19.2%; Pred. No. 2.4;
Matches 56; Conservative 32; Mismatches
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Best Local Similarity 22.01
Matches 69; Conservative
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Glucan 1,3-beta-glucosidase (EC 3.2.1.58) - yeast (Saccharomyces cerevisiae)

N.Alternate names: exo-1,3-beta-glucosidase; protein YD9320A.12c; protein YDR261C
C; Species Saccharomyces cerevisiae
C; Species Saccharomyces cerevisiae
C; Species Saccharomyces cerevisiae
C; Accession: 555516; 867319; 867464
R; Correa, J.; Varquaz de Aldana, C.; San Segundo, P.; del Rey, F.
R; Correa, J.; Varquaz de Aldana, C.; San Segundo, P.; del Rey, F.
A; Description: EXG2, a gene coding for a exo-1,3-B-glucanase with a GPI anchor attachmen A; Reference number: 855516
A; Molecule type: DNA
A; Reference number: 855516
A; Molecule type: DNA
A; Residues: 1-562 - CCNA
A; Cross-references: EMBL: Z46870; NID: G861116; PIDN: CAA86950.1; PID: G861117
A; Experimental source: strain AB320
R; Murphy, L.; Harris, D.
R; Murphy, L.; Harris, D.
R; Murphy, L.; Harris, D.
R; Murphy, L.; Harris, D.
R; Murphy, L.; Marris, D.
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A;Residues: 1-562 <MUR>
A;Cross-references: RMBL:Z68329; NID:gl136205; PIDN:CAA92719.1; PID:e215308; PID:gl13621
R;Murphy, L.; Harris, D.
submitted to the EMBL Data Library, March 1996
A;Reference number: S67454
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A;Residues: 1-562 <MUM>
A;Cross-references: EMBL:Z70202; NID:g1226026; PIDN:CAA94100.1; PID:e228630; PID:g122603
C;Genetics:
                                                                                                                                                                                                                    232 ---DWLEKDLTQARNEGKAIILNYHDSDNNW-----KNNYAPATYEQLKARRSDILKKY 282
-YLGLSLHYLGDVNQPMHAANFTNLSYPMGFHSKYENFVDTIKNNYIVSDSNGYWNWKGA 207
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                                               208 NPEDWIEGAAVAAKQDYPGVV---NDTTKDWFVKAAVSQEYA----DKWRAEVTPVTGKR
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Search completed: July 27, 2004, 14:47:48 Job time : 18 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 atgaaaaagaaagtattagc......8tacgtatgtaaatcgctaa 849 6940544 3470272 segs, 21671516995 residues Total number of hits satisfying chosen parameters: IDENTITY NUC Gapop 10.0 , Gapext 1.0 PCT-US03-12556-1 Title: Perfect score: Seguence: Scoring table: Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 1
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BCT 02-0CT-1998 BTY16268

Bacillus thuringiensis plcA gene and partial plcB gene and partial plcB gene and partial plcB gene at 186268

Y16268.1 GI:2815226
phospholipase C; plcA gene; plcB gene; sphingomyelinase.
Bacillus thuringiensis
Bacillus thuringiensis
Bacillus thuringiensis
Bacillus thuringiensis

cereus group.

Lovgren,A., Carlson,C.R., Eskils,K. and Kolsto,A.B. Localization of putative virulence genes on a physical map of the bacillus thuringiensis subsp. gelechiae chromosome

AUTHORS TITLE REFERENCE

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Gilmore, M.S., Cruz-Rodz, A.L., Leimeister-Wachter, M., Kreft, J. and
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A Bacillus cereus cytolytic determinant, cereolysin AB, which comparises the phospholipase C and sphingomyelinase genes: nucleotide sequence and genetic linkage
J. Bacteriol. 171 (2), 744-753 (1989)
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PDTYGNR"
                                                                                                  Direct Submission
Submitted (21-JAN-1998) A. Lovgren, Dept of Microbiology, Stockholm
University, S-106 91 Stockholm 106 91, SWEDEN
Location/Qualifiers
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|transl_table=11
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                                                                                                                                                                                                           1. 1675
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Best Local Similarity
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TRASHEYDDDNGKTY I PFAKQAKETGAKY FKLAGESYKNKOKQAFFLGSLHJYLGD
VNQPMHAARTNLSY PCQFFISKY ENEVDT IKONYKYTDGNGYMNMKGTNPERIHGAA
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                                                                                                                                                                                                                                                                        26-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 2349)
Gavrilenko, I.V., Baida, G.E., Karpov, A.V. and Kuz'min, N.P.
Nuclectide sequence of phospholipase C and sphingomyelinase genes
Trom Bacillus cereus BKM-B164
Bioorg. Khim. 19 (1), 133-138 (1993)
                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kuzmin, N.P.
Direct Submission
Submitted (14-JAN-1992) N.P. Kuzmin, Inst. of Biochemistry &
Physiology of Microorganisms AS USSR, Pustchino, MOSCOW Region,
142292, USSR
                    GCCGTATCTCAAGAATATGCAGATAAATGGCGTGCGGAAGTAACACCGGTGACAGGAAAG
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phospholipase C; PLC gene; sph gene; sphingomyelinase.
Bacillus cereus
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53. .904
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sph.
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FDTYGNR"
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Larity 79.1%; Pred. No. 1.1e-104;
Conservative 0; Mismatches 175;
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VVARQDYGGGTVNDNTKDWFVKRAVSQEYADKWRAEVTPWTGKRLMDAQRVTAGYIQLW

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1 (bases 1 to 2050)
Johansen,T., Holm,T., Guddal,P.H., Sletten,K., Haugli,F.B.
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Johansen,T., Haugli,F.B., Ikezawa,H. and Little,C.
Bacillus cereus strain SE-1: nucleotide sequence of
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/note="put. signal peptide (PLC)
676. .1410
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1102 TCTAAATATGAAAACTTTGTAGATACGATAAAAGATAATTATAAAGTAAGGATGGAAT 1161
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Nuclectide sequence of phospholipase C and sphingomyelinase genes
from Bacillus cereus BKM-B164
Bloorg. Khim. 19 (1), 133-138 (1993)
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Kuzmin,N.P.
Direct Submission
Submitted (14-JAN-1992) N.P. Kuzmin, Inst. of Biochemistry & Physiology of Microorganisms AS USSR, Pustchino, MOSCOW Region, 142292, USSR
                                                                                                   GCTAAACAAGATTATCCTGGCGTTGTGAACGATACGACAAAAGATTGGTTTGTAAAAGCA
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B.cereus fuse genes plc and sph (=h-cerAB).
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Bacillus cereus
Bacillus cereus
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/gene="h-cerAB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="pot. rho-independent terminator"
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Read, T. Peterson, S., Tourasse, N., Baillie, L., Paulsen, I., Nelson, K., Tettelin, H., Fouts, D., Eisen, J., Gill, S., Holtzapple, E., Okstad, O., Helgason, E., Riletone, J., Mu, M., Kolonay, J., Beanan, M., Dodson, R., Brinkac, L., Gwinn, M., DeBoy, R., Madupu, R., Daugherty, S., Durkin, A., Haft, D., Nelson, W., Peterson, J., Pop, M., Khouri, H., Berton, J., Mahamoud, Y., Jang, L., Hance, T., Weidman, J., Berton, J., Pop, K., Plaut, R., Wolf, A., Watkins, K., Nierman, W., Hazen, A., Thomason, B., Friedlander, A., Koehler, T., Hanna, P., Kolsto, A.-B. and
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1 (Dases I to 290214)

Read, T., Peterson, S., Tourasse, N., Baillie, L., Paulsen, I.,
Read, T., Peterson, S., Tourasse, N., Eisen, J., Gill, S., Holtzapple, E.,
Nelson, K., Tettelin, H., Fouts, D., Eisen, J., Gill, S., Holtzapple, E.,
Okstad, O., Helgaeon, E., Rilstone, J., Mi, M., Kolonay, J., Baenan, M.,
Dodson, R., Haft, D., Nelson, W., Peterson, J., Pop, M., Khouri, H.,
Radune, D., Benton, J., Mahamoud, Y., Jiang, L., Hance, T., Weidman, J.,
Berry, K., Plaut, R., Wolf, A., Watkins, K., Nierman, W., Hazen, A.,
Cline, R., Redmond, C., Thwaite, J., White, O., Salzberg, S.,
Thomason, B., Friedlander, A., Koehler, T., Hanna, P., Kolsto, A.-B. and
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Bacillus anthracis str. Ames
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
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Nature 423 (6935), 81-86 (2003)
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Direct Submission
Submitted (26-MAR-2003) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
                                                                      778 CGITITAAIGGAAGCGCAGCGCGITACAGCIGGITATAITCATTIGIGGITIGAIACGIAI
                                             718 GCCGTATCTCAAGAATATGCAGATAAATGGCGTGCGGAAGTAACACCCGGTGACAGGAAAG
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VNQPMHAANFTNLSYPQGFHSKYENPYDTIKDNYKYTDGNGYMWKGTNBEBWIHGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGATATTGGAATTGGAAAGGAGCAAACCCAGAAGATTGGATTGAAGGAGCAGCGGTAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 GCGAAACATGCAAAAGAAACAGGCGCAAAATATTTTAACCTTGCTGGTCAAGCATACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGCGTGCTGATTTAGAAAATGGTATTTATTCTGCTGATTACGAGAATCCTTATTATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 TGGCGTACGGAGTTAGAGAACGGTATTTATGCTGCTGACTATGAAATCCTTATTATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATAGTACATATGCTTCTCACTTTTATGATCCGGATACTGGAACAACATATATTCCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rctaaatatgaaaactttigtagatacgataaaagataattataaagtaacggatggaaat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGAAAAAGAAAGTATTAGCACTAGCAGCTATGGTTGCTTTAGCTGCGCCAGTTCAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGAGGATAAGCATAATGAGGGGATTAACTCTCATTTGTGGATTGTAAATCGTGCAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 gergaagaraacaraaagaagargraarrerearrrargaargaaacgracgracarr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 GACATCATGTCTCGTAATACAACGATTGTGAATCCGAATGAAACTGCATTATTAAATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418 AATCAAGATATGCAGCAAGCATTCTTCTACTTAGGATTATCGCTTCATTATTAGGAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 2201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 554; DB 1; Length 22
Pred. No. 2.8e-104;
0; Mismatches 175; Indels
                                                                                                                                                                                                                                                 Note="structural part of gene plc" evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                    918. 1828
/gene="h-cerAB"
/note="etructural part of gene sph"
/evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                evidence-experimental
                                                                                                                                                                                                             53. .899
/gene="h-cerAB"
                                                                                                                                                                                                                                                                                                                     gene="h-cerAB"
'note="linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 79.1%;
Matches 672; Conservative C
                                                                                                                                                                                                                                                                                                   900
                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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AITVGASYTKKLPADMIGGRAVIAMYSPSEGNEVQRESPASKIMNVKIGVIPLPLYVVLA
AITVGASYTKKLPADMIGGRAVIMINGIFLGDIGKRIPTILKNIGGRALLSLETPSLLV
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FANNANGLAVGSLEGERKHTRFFFITVPIVSGGIGGGILPLSLAVSDILNESSATFVS
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ESAIVTGCHSGLGGTGDVAILSASNRMELMPFAQISTRLGGAAMVVTATILLKMFS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESCKAIAADEETVYDYTARGIMWAVVSDGTAVLGLGNIGPKAAMPVMEGKSILFKKFA
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SLNGRVFTTDEMAQLVGISRVSIRKYVMFLTDIGVLENEMMYQHVGRPVSKLRCVDQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /trānslation="MKKIGTMLLFSILJAGCTQAQPDLKKPKKEAIATSSTQVNAPSF
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PID:1786892; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (9996. .10922)
locus tag="BA0581"
'note="identified by match to PFAM protein family HMM'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and GP:10173012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.1%; Score 552.8; DB 1; Length 290214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7861. -9060
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/note="similar to GP:10173012, and GP:101730
identified by sequence similarity; putative"
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/db_xref="GI:30254184"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="transporter, EamA family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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/db_xref="GI:30254186"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (9996. .10922)
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6455. .7801
                                                                                                                                                                                                                                                                                                                                                                    locus_tag="BA0578"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (9356.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'codon_start=1
'transī_table=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon start=1
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                                                                                                                                                                                                                                                                                 .7801
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                                                                                                                                                                                                                                                                                          gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MMMVFTIGVMSLSILGGASPSETSKGKTDYKQRSKEQLANGKIH
KWYTEEKAEKLGIETTGKEQITLEKEIHETEVGREAKQLGISTEKOVGTLSEBIYET
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REBAGKLGISPKGKEIEVLAQEVYEGKVQEEKKEYHLDLYGKDIYQVLSEINGKVLQ
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DGVRGNPNBGFVGNIYTFSSGSYGVHGPLFQLAKKYLPNKAVDLTGKSIEELYKSVK
AGQPVVIITNATFABLBDEFTTWETNNGDVSITYNEHCVVLIGYDQESVYIRDPLKD
SLDVKVPREKFEQAWVQMGSQAISYVKRSK"
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TMLOSVKEGIIAVDKAARVTLINNEARLFKKSGLEEDFIGKDVELYMPNSRIKEVLO
TGEVQLMEBERONIYGIITUYNRVPLYVKEEIVOALATRROKTER RKLAEBELTGIRLYAE
ALAAOSHEPMIKM-VLGITHWKQY EELOKY ISGWGSHQYBE IGGWKRIKSPYPAGF
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EVKIQHEDILTITVQDTGKGIQEKEIEBLFTKGYSTKGDNRGYGLYLVKESIQRINGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QAEKAKTIAHIVANDSIVIDGLIGKADTSAIQTYTNRILKNTGVQFIVVMDMNGIRKS
HPNPQKIGHHFIGGDEGPALKGKEHVSLAEGTIGISMRVFVPIPSETGEQLGAVAVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MKKRKRLWNLWKTITLLVCTVVIFSLLVTDILISHNVERTTEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /locus tag="BA0577"
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similarity; putative"
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963. 1709
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68:X04830, and PID:42533; identified by sequence similarity; putative"
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GB:214244, SP:P24311, and PID:30151; identified by
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db xref="GI:30254181"
                                                                                                                                                                                                                                                                                                                                                                                         product = "conserved hypothetical protein"
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db_xref = "GI:30254180"
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protein id="AAP24596.1"
db_xref="GI:30254182"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IHMHSLVGKGTTITIEIPKGRDERQI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            locus_tag="BA0575"
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                                                                                                                                                                                                                                                                                                                                                                          table=11
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trans table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1963. .3945
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                                                                                                                                              gene
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CDS

CDS

gene

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DIAVGLGVPLTKSRVPMLLLSGTALIGGAVARAGGIGFVGLMPRISFRLVGSLVGLLI
PVAAIVGAILVLAADLIGRTIFTPLEIPAGVFTSAIGAPYFIYLLYKSRNS"
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/dc xref="G1:28894544"

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/note="similar to Iron(III) dicitrate transport system
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/product="Iron(III) dicitrate-binding protein"
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NDVATIEKVAFASDLMPLARDGRVSEEAASIRGIIDACDLGVYIPVMRAIERSIIAK
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                                                                                                                                                                                                                                                                                                                                                                                                         SSONDGAYGKYNTGASHTFKEARKPNPDEKKDYOAIKSVVNKDVKELKKIIEKTIENK
TNANSDKYYGRLRKKPLRIYTEKOPRMFYKKGGESOELDVAFQLLVDCSGSMYNKMEE
TKKSVVLFHEALKSLKIPHAISGFWEDASSAKPEDKPNVIHEVVNYKNSTLPNVGPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MQLREEBDNRDGYIIRIVSEKLAKRPEKHKFLLVFTDGEPSALDYQQDGILDTHEAVK
LARKSGMEVIGIFIEEGEAKEATYQLMKNIYNHFLVANHAEDLRLKIKPLLKKLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MLEQFHIHADLKQQLSTIHEKNKQEAGENAHLIGTKIYKASDNS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTAGTATTTGCACAAACAATAATAGTG---AAAGTCCTGCACCGATTTTAAGATGGTCA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTGAGGATAAGCATAATGAGGGGATTAACTCTCATTTGTGGATTGTAAATCGTGCAATT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                         factor type A domain protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60306 ATGAAAAAAAGTACTTGCTTTAGCGGCAGCTATTACATTAGTTGCTCCATTACAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60366 GTTGCATTTGCTCATGAAATGATGAGGGGACAGAATTTGGAGTTATTCGGCGCTGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACATCATGTCTCGTAATACAACGATTGTGAATCCGAATGAAACTGCATTATTAAATGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60546 receracreaerradaeaacecrarranecrecreacrareaaarcerrarrar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGAAAAAGAAAGTATTAGCACTAGCAGCTATGGTTGCTTTTAGCTGCGCCAGTTCAAAGT
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AVEWVDRTIANERPPYYDGGFEYLLEVAIPYKFQPETK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transī_table=11
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complement (9837. .10730)
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EC number-"
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/trans] table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGKGAGTVKHFGLSDKVDFQIGTLSKAIGVIGGYVAGKQNLIDWLKVRSRPFLFSTAL
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EALIREVKEETGLTATLGGLVAINEKFFEESGNHALFFTFRANVEKGELIAEDEGEIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWPNSIDATAAMKEWGFKAEYDLDKMTTDMLAKLKKKLTAELVMN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IYPQDEBEYKRRLRI PLFLLFSCTK'
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complement (4285. .5016)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              table=11
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'transT table=
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transl_table=
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/transl_table=
                                                                                                protein fecE'
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YMLSTYLIYPWWGQTERADLIGAADYIKWQDVVILNEVPDNSASDRLIGULKKEYPWQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGAAGATAAACATAAAGAAGGCGTGAATTCTCATTTATGGATTGTAAACCGTGCAATT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACATCATGTCTCGTAATACAACGATTGTGAATCCGAATGAAACTGCATTATTAAATGAG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATATTATGICICGIAATAAAGACTTGIAAAACAAGATCGAGTTGCACTATTAAATGAA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGCGTGCTGATTTAGAAAATGGTATTTATTCTGCTGATTACGAGAATCCTTATTATGAT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATAGTACATATGCTTCTCACTTTTATGATCCGGATACTGGAACAACATATATTCCTTTT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGAAACATGCAAAAGAAACAGGCGCAAAATATTTTAACCTTGCTGGTCAAGCATACCAA 417
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frans1_table=1.1
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protein id="#AA040751.1"
db_xref="GI:28414376"
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organism="Bacillus cereus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="sphingomyelinase"
'codon start=1
'transT_table=11
                   /mol_type="genomic DNA"
/strain="569"
                                                                                                                                                                                                                                                                                                                                                                                          complement (1085. .1103
                                                      /db_xref="taxon:1396"
                                                                                                                                                                                                                                                                                                                                                                                                              /note="putative"
/bound_moiety="PlcR"
                                                                           12. ... 57
/bound_moiety="PlcR"
                                                                                                                               /gene="pc-plc"
181. .1032
                                                                                                                                                                    gene="pc-plc"
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/gene="sph"
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Bacillus cereus strain 569 phosphatidylcholine-specific
hospholipase C (pc-plc) and sphingomyelin-specific phospholipase (sph)
AY195600
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                                                         GCGAAACATGCAAAAGAAACAGGCGCAAAATATTTTAACCTTGCTGGTCAAGCATACCAA
                                                                                              50666 GCAAAGCAAAGCAAAGGAAACAGGAGCTAAATATTTTAAATTAGCTGGTGAGTCTTATAAA
                                                                                                                                   AATCAAGATATGCAGCAAGCATTCTTCTAGGATTATCGCTTCATTATTTAGGAGAT
                                                                                                                                                                    AATAAAGATATGAAACAAGCGTTCTTCTATTTAGGATTATCTCTTCATTATTTAGGGGAT
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Direct Submission
Submitsed (11.DEC-2002) NIAID, NIH, 30 Convent Dri
Bethedda, MD 20892, USA
3 (bases 1 to 2130)
Pomerantsev, A.P., Kalnin, K.V. and Leppla, S.H.
Direct Submission
Submitted (19-FEB-2003) NIAID, NIH, 30 Convent Dri
Bethedda, MD 20892, USA
Sequence update by submitter
On Feb 19, 2003 this sequence version replaced gi:
Location/Qualifiers
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/tränslation="WKGKLLKGVLSLCOVGLGALYSGTSAQAEASTNQNDTLKVMTHNV
YMLSTNLYPWWGQTERADLIGAADYIKNQDVVILNEVPDNSASDRLLGNLKKEYPNQT
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YYKIKKURDREVHVIGTHLQAEDSMCGKTSPAASVRTNOLKETODFIKNNIPNNERYL
IGGDNAVNKINAENNNDSBYASMFKTLAASVPSYTGHTATWDATTNSIAKYPEDDSPA
BYLDYIIASKDHANPSYIENKVLQPKSPQWTVTSWFQKYTYNDYSDDYPVEATISMK"
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hemolysin.
Bacillus cereus
Bacitlus cereus
Bacteria; Firmicutes; Bacillales; Bacillus; Bacillus
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/product="sphingomyelinase (AA 1 - 306)"
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                                                                                                                                                                                       'note="signal peptide (AA -27 to -1)"
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Pred. No. 1e-42;
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/note="pot. ribosome binding
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                                                                                                      388. .404
/note="inverted repeat A'"
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/note="inverted repeat B'"
                                                 'note="inverted repeat A"
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partial
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163. .368
'note="-35 region"
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/note="-10 region"
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B.cereus hemolysin gene,
M35411
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82.1%;
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Matches 294; Conservative
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VTAGYIQLWFDTYGNR...
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Manda,A., Tsukagoshi,N., Udaka,S., Sasaki,T., Makino,S.,
Nakamura,S., Little,C., Tomita,M. and Ikezawa,H.
Nucleotide sequence and expression in Escherichia coli of the gene coding for sphingomyelinase of Bacillus cereus
Eur. J. Blochem. 175 (2), 213-220 (1988)
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                                                                                                                                                                                                                                                                                                GCTAAACAAGATTATCCTGGCGTTGTGAACGATACGACAAAAGATTGGTTTGTAAAAGCA 717
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus,
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phospholipase; phospholipase C; serine carboxypeptidase;
sphingomyelinase.
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CTDDVSEWFHENAKRAQADYPKIVNTIKKSYIQGLSDSGKORTWKKAVRATGKRL"
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20.8%; Score 176.8; DB 1; Length 825;
Best Local Similarity 52.3%; Pred. No. 2e-26;
Matches 391; Conservative 0; Mismatches 357; Indels 0
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1. .>825
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1 (bases I to 280)
Gilmore, M.S., Gilmore, K.S. and Goebel, W.
A new strategy for ordered DNA sequencing based on a novel method for the rapid purification of near-milligram quantities of a cloned Gene Anal. Tech. 2, 108-114 (1985)
Original source text: B.cereus DNA.
Location/Qualifiers
                                                                                                                                                                                                                                                  /cransI_table=11
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Listeria seeligeri phospholipase (plcB) gene, partial cds.
AY150839
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Watcher, M., Schmid, M. and Wagner, M.
Direct Submissor.
Bubmitted (11-SEP-2002) Lehrstuhl fuer Mikrobiologie, Am Hochanger
4, Freising 85354, Germany
1. Freising 88384
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid-based, cultivation-independent detection of Listeria
Bpp. and genotypes of L. monocytogenes
FEMS Immunol. Med. Microbiol. 35 (3), 215-225 (2003)
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Listeria seeligeri
Bacteria, Firmicutes, Bacillales; Listeriaceae; Listeria.
1 (bases 1 to 825)
Schnid, M., Walcher, M., Bubert, A., Wagner, M., Wagner, M. and Schleifer, K.H.
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                                                                                                                                                                                                                                      codon start=2
transl_table=
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Best Local Similarity 79.95
Matches 223; Conservative
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Corganism="Listeria monocytogenes EGD-e"
/mol_type="unassigned DNA"
/db_xref="taxon:169963"
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Listeria inocus, genome and applications
Patent: WO 0228891-A 2646 11-APR-2002;
INSTITUT PASTEUR (FR); CENTRE NATIONAL DE
SCIENTIFIQUE (CNRS) (FR)
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Pred. No. 8.2e-22;
); Mismatches 291;
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Matches 329; Conservative 0
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Listeria monocytogenes EGD-e
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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Patent: WO 022891-A 740 11-APR-2002;
INSTITUT PASTEUR (FR); CENTRE NATIONAL DE
SCIENTIPQUE (CNRS) (FR)
Location/Qualifiers
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WO0228891.
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AX413749
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ilarity 53.1%; Pred. No. 6.8e-22;
Conservative 0; Mismatches 291;
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                                                                                                                                                                                                                                                                                                                                                                                                                  complement (4493. .5167)
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                                                                                                                                                                                                                                                                                                        lactate dehydrogenase, lecithinase, surface antigen.
Listeria monocytogenes
Listeria monocytogenes
Bacteria, firmicutes, Bacillales, Listeriaces, Listeria.
I (bases I to 5648)
Vazquez-Boland, J.A., Kocks, C., Dramsi, S., Ohayon, H., Geoffroy, C., Mengaud, J. and Cossart, P.
Morlectide sequence of the lecithinase operon of Listeria monocytogenes and possible role of lecithinase in cell-to-cell
                                                                                                  LISACTLDH
LISTERIA MONOCYTOGENES lecithinase, lactate dehydrogenase (actA)
gene complete cds, (plcB) gene complete cds, (ldh) gene complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Listeria monocytogenes"
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92104678
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M82881.1 GI:149644
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VERSION
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AUTHORS
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AKTIIGDNVFVGCNSNLIAPVKVGDRAFIAAGSTITKDVPEDALGIARAKQDNKLGYY
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                                                                                                                                                                                                                                                                                             160050 bp DNA linear BCT 06-JUN-2002
Listeria monocytogenes strain EGD, complete genome, segment 2/12.
AL591974 AL591824
AL591974.1 GI:16409560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glaser, P., Frangeul, L., Buchrieser, C., Rusniok, C., Amend, A., Baquero, F., Berche, P., Bloecker, H., Brandt, P., Chakraborty, T., Charbit, A., Chetouani, F., Couve, E., de Daruvar, A., Dehoux, P., Domann, E., Dominguez-Bernal, G., Duchaud, E., Durant, L., Dussurget, O., Entian, K.D., Fsihi, H., Portillo, F.G., Garrido, P., Jackson, D., Jones, L.M., Kaerst, U., Kreft, J., Kuhn, M., Kunst, F., Jackson, D., Jones, L.M., Raerst, U., Kreft, J., Kuhn, M., Kunst, F., Sturapkat, G., Madueno, E., Mattournan, A., Vicente, J.M., Nay, E., Nedjari, H., Nordsiek, G., Novella, S., de Pablos, B., Perez-Diáz, J.C., Purcell, R., Remmel, B., Rose, M., Schlueter, T., Simoes, N., Tierrez, A., Vazquez-Boland, J.A., Voss, H., Wehland, J. and Cossart, P. Comparative genomics of Listeria species
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Direct Submission
Submitted (06-JUN-2001) Glaser P., Institut Pasteur, Genomique des
Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris
Cedex 15, FRANCE
E-mail: pglaser@pasteur.fr
Phone: +33 1 45 68 89 96, Fax: +33 (0)1 45 68 87 86.
                                                                             697
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Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
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MEDLINE
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:TKLTSISENGTIMNLQYYKGAFVIMSGFIDTETSVGYYNLEVISEQATAYVIKINEL
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11743
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DB 1; Length 160050;

Query Match 18.2%; Score 154.4; DB 1; Length Best Local Similarity 53.1%; Pred. No. 4.9e-22; Matches 329; Conservative 0; Mismatches 291; Indels

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August 2, 2004, 02:14:50 ; Search time 483 Seconds (without alignments) 8618.563 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 740, App Sequence 2646, Ap Sequence 31, Appl Sequence 97, Appl Sequence 97, Appl Sequence 81, Appl Sequence 81, Appl Sequence 470, App Sequence 470, Appl Sequence 470, Appl US-10-421-654-1 US-10-169-493-40434 US-10-421-654-3 US-10-421-654-5 US-10-398-221-740 6 US-10-398-221-2646 6 US-10-421-654-31 6 US-10-421-654-97 6 US-10-421-654-97 6 US-10-421-654-97 6 US-10-421-654-97 6 US-10-398-221-3772 US-10-398-221-3772 US-10-398-221-3772 US-10-398-221-3772 US-10-398-221-3772 US-10-398-221-3772 US-10-398-221-3772 100.0 65.9 65.9 62.3 59.6 18.2 10.3 849 559.2 529 529 1154.4 1

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	US-10-429-034-21	US-08-781-986A-13	329	240	260	311.	US-10-240-589C-6	US-10-067-385-7	158	769	282	US-10-398-221-8	US-10-398-221-2	US-10-312-841-2	US-10-094-240-10	US-10-056-405-10	424	282	US-09-815-242-431	15-	349.	282	US-10-312-841-1	221	311.	US-10-341-434-82	322.	029	US-10-311-455-59	US-09-790-988-1	US-10-441-926-7
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•	3.2	43.2	3.2	43	41.8	41.8	41.8	41.6	1.6	1.6	41.6	1.6	41.6	41.2	41	41	40.4	40.2	40	40	9.6	9.8	9.6	9.4	9.2	9.2	9.2	33	39	39	38.8
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ALIGNMENTS

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                                    Sequence 1, Application US/10421654
Fublication No. US20040005604A1
Fublication No. US20040005604A1
GENERAL INFORMATION:
APPLICANT: Gramatikova, Svetlana
APPLICANT: Hallewood, Geoff
APPLICANT: Lam, David E.
APPLICANT: Barton, Nelson R.
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM AND TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 09010-094001;
CURRENT APPLICATION NUMBER: US/10/421,654
CURRENT FILING DATE: 2003-04-21
PRIOR FILING DATE: 2002-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGAAAAAGAAAGTATTAGCACTAGCAGCTATGGTTGCTTTAGCTGCGCCAGTTCAAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-421-654-1
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 849; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Unknown
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RESULT 1
US-10-421-654-1
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RESULT 3
US-10-421-654-3
; Sequence 3, Application US/10421654
; LENGTH: 1192
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-369-493-40434
                                                  Query Match
Best Local Similarity 79.3%;
Matches 676; Conservative
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| Sequence 40434, Application US/10369493
| Sequence 40434, Application US/10369493
| Publication No. U820030233675A1
| Publication No. U820030233675A1
| APPLICANT: Cac, Yongwei
| APPLICANT: Gladman, Barry S. APPLICANT: Gladman, Barry S. APPLICANT: Gladman, Barry S. APPLICANT: Gladman, Barry S. APPLICANT: Gladman, Barry S. APPLICANT: Gladman, Barry S. APPLICANT: Gladman, Barry S. APPLICANT: Gladman, Barry S. APPLICANT: Gladman, Barry S. APPLICANT: Gladman, Barry S. APPLICANT: Gladman, Barry S. APPLICANT: Gladman, Barry S. APPLICANT: Gladman, Barry S. APPLICANT: US/10/369,493
| TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
| TITLE REFERENCE: 38-10(52052)B |
| CURRENT FILING DATE: 2003-02-28 |
| PRIOR APPLICATION NUMBER: US 60/360,039 |
| PRIOR APPLICATION NUMBER: US 60/360,039 |
| WUMBER OF SEQ ID NOS: 47374 |
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781 CGTTTAATGGATGCACAACGTGTTACTGCTGGATACATTCAGCTTTGGTTTGATACGTAC 840
                                                                                                                            GTAGTATTTGCACAAACAAATAATAGTG---AAAGTCCTGCACCGATTTTAAGATGGTCA 117
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                                                                                              1 ATGAAAAAGAAAGTACTTGCTTTAGCGGCAGCTATTACATTAGTTGCTCCATTACAAAGT
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                                                            1 ATGAAAAAGAAAGTATTAGCACTAGCAGCTATGGTTGCTTTAGCTGCGCCAGTTCAAAGT
                              Gaps
                                3,
DB 16; Length 1192;
                              Indels
Score 559.2; DB 16;
Pred. No. 1.7e-125;
0; Mismatches 173;
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840

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AAAGCTGATTTTCCATCAATTGTTAATGATAAGACGAAAAATTGGTTCCTAAAAGCAGCT 720
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                                                                                                                                                                                                                                                                                              Sequence 5. Application US/10421654

| Sequence 5. Application US/10421654
| Publication No. US20040005604A1
| GENERAL INFORMATION:
| APPLICANT: Gramatikova, Svetlana
| APPLICANT: Hazlewood, Geoff
| APPLICANT: Hazlewood, Geoff
| APPLICANT: Barton, Nelson R.
| TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM APPLICANT: Barton, Nelson R.
| TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM APPLICANT: 20010-094001
| CURRENT FILING DATE: 2003-04-21
| PRIOR PLLING DATE: 2003-04-12
| PRIOR PLLING DATE: 2003-04-19
| PRIOR PLLING DATE: 2002-04-19
| NUMBER OF SEQ ID NOS: 106
| SOFTWARE: FastSEQ for Windows Version 4.0
                                                             TTAATGGAAGCGCAGCGCGTTACAGCTGGTTATATTCATTTGTGGTTTGATACGTATGTA
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OTHER INFORMATION: Obtained from an environmental sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.6%; Score 505.8; DB 16; 75.7%; Pred. No. 1.4e-112; ive 0; Mismatches 197; 1
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ORGANISM: Unknown
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US-10-421-654-5
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                                                                                                            ACIDS ENCODING THEM AND USING THEM
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 62.3%; Score 529; DB 16; I
Best Local Similarity 76.4%; Pred. No. 3.2e-118;
Matches 649; Conservative 0; Mismatches 200;
                            APPLICANT: Hazlewood, Geoff
APPLICANT: Hazlewood, Geoff
APPLICANT: Hazlewood, Geoff
APPLICANT: Hazlewood, Geoff
APPLICANT: Jam. David E.
APPLICANT: Barton, Nelson R.
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACTI
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACTI
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACTI
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACTI
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACTI
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACTI
TITLE OF INVENTION: DATE: 2003-04-21
PRIOR APPLICATION NUMBER: US 60/374,313
PRIOR APPLICATION NUMBER: US 60/374,313
PRIOR PILING DATE: 2002-04-19
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1852
Publication No. US20040005604A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Unknown
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US-10-421-654-3
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320 ATADAAATCCATATTATGATACTAGTACATTTTTATCATTTTTATAAATCCTGATAGAG 379
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                                                                    GAACAACATATATTCCTTTTGCGAAACATGCAAAAGAAACAGGCGCAAAATATTTAAACC
                                                                                                      380 ATAATACTIATTIGCGGGTTTTGCTAATGCGAAAATAACAGGAGCAAAGTATTTCAATC
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APPLICANT: GLASER, Philippe
1 TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT PILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR APPLICATION NUMBER: PC 00/12 697
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR APPLICATION NUMBER: PC 00-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: Patentin Version 3.0
SEQ ID 02646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 154.4; DB 16; Length 870;
Pred. No. 3.3e-27;
0; Mismatches 291; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Listeria monocytogenes EGDe
US-10-398-221-2646
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US-10-398-221-2646
US-10-398-221-2646, Application US/10398221
Publication No. US20040018514A1
GENERAL INFORMATION:
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Best Local Similarity 53.1%;
Matches 329; Conservative (
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    CAAGATATGCAGCAAGCATTCTTCTACTTAGGATTATCGCTTCATTATTAGGAGATGTG 480
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                                 412 AAAGATCTGAAAAATGCATTCTTTTTTTAGGATTATCACTTCATTATTTAGGGATGCC
                                                                                                                         TATTGGAATTGGAAAGGAGCAAACCCAGAAGATTGGATTGAAGGAGCAGCGGTAGCAGCT
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/ Sequence 740, Application US/10398221

/ Publication No. US20040018514A1

/ Publication No. US20040018514A1

/ APPLICANT: KUNST, Frederik

/ APPLICANT: KUNST, Frederik

/ APPLICANT: GLASER, Philippe

/ TTLE OF INVENTION: Listeria innocua, genome and applications

/ TTLE REFERENCE: 344 702 - US

/ CURRENT FILING DATE: 2003-03-27

/ PRIOR FILING DATE: 2001-10-04

/ PRIOR FILING DATE: 2001-10-04

/ NUMBER OF SEQ ID NOS: 4025

/ SEQ ID NO 740

/ LENGTH: 970
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18.2%; Score 154.4; DB 16; Length 870;
Best Local Similarity 53.1%; Pred. No. 3.3e-27;
Matches 329; Conservative 0; Mismatches 291; Indels 0;
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1 ORGANISM: Listeria monocytogenes-EGD
US-10-398-221-740
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SOFTWARE: FastSEQ for Windows Version 4.0
  ATGCATGCAGCAAACTTTACGAATCT
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Publication No. US20040005604A1
STRERAL INFORMATION:
APPLICANT: Gramatikova, Svetlana
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10.1%; Scc
Best Local Similarity 53.1%; Pre
Matches 283; Conservative 0;
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320 ATAAAATCCATATTATGATACTAGTACATTTTTATCTCATTTTTATAATCCTGATAGAG 379
                                                                             398 TIGCTGGTCAAGCATACCAAAATCAAGATATGCAGCAAGCATTCTTCTACTTAGGATTAT 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTATGAAAATGCGAAAAGGGGGAAAGCGGACTACCCGAAAATAGTCAATGCGAAAACTA 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ## Sequence 31, Application US/10421654

## Sequence 31, Application US/10421654

## Publication No. US20040005604A1

## Sequence 31, Application US/20040005604A1

## Publication No. US20040005604A1

## APPLICANT: Gramatikova, Svetlana

## APPLICANT: Harlewood, Geoff

## APPLICANT: Harlewood, Geoff

## APPLICANT: Harlewood, Geoff

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## APPLICANT: Lam, David E.

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## APPLICANT: Lam, David
                                              338 GAACAACATATATTCCTTTTGCGAAACATGCAAAAGAAACAGGCGCAAAATATTTTAACC
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ORGANISM: Unknown
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489 --TTCTTATCCAATGGGTTTCCATTCTAAATAC 546 999 AATTTG-----GTCAATTCTGATGATCCGAAGCAGTGGATACATGAAACAGCGAAACTC 738 GATTATCCTGGCGTTGTGAACGATACGACAAAAGATTGGTTTGTAAAAGCAGCCGTATCT 726 739 GCAAAAGCAGAAATTATGAATATTACTAGTGATAA-----TATTAAATCTCAATATAAT 792 727 CAAGAATATGCAGATAAATGGCGTGCGGAAGTAACACCGGTGACAGGAAAGCGTTTAATG 786 793 AAAGGAAACAAAGATCTTTGGCAACAAGAAGTTATGCCAGCTGTCCAGAGGAGTTTAGAG 852 313 TCTCACTTTTATGATCCGGATACTGGAACAACATATATTCCTTTTGCGAAACATGCAAAA 372 385 TCTCATTTCTACGATCCCGATACAAGAAGAACTATAAAGGGGAGGAAGAACCAACAGCT 444 373 GAAAC---AGGCGCAAAATATTTTAACCTTGCTGGTCAAGCATACCAAAATCAAGATATG 429 445 CTTTCTCAAGGAGATAAAATATTTTAAATTAGCAGGTGAATACTTTAAGAAGAAGAATGATTGG 504 564 ATGCATGCAGCAAACTTTACGAATCT---TTCTTATCCAATGGGTTTCCATTCTAAATAC 546 Argeniscriscriatificascristcsacassasiscrataaastricatasiscritt 624 AATTGGAAAGGAGCAAACCCAGAAGATTGGATTGAAGGAGCAGCGGTAGCAACTAAACAA GAAAATTTTGTTGATACAATAAAAATAACTATATTGTTTCAGATAGCAATGGATATTGG ATGCATGCTGCTAATTTTACAGCTGTCGACATGAGTGCAATAAAGTTTCATAGCGCTTTTT CAGCAAGCATTCTTCTACTTAGGATTATCGCTTCATTATTTAGGAGATGTGAATCAGCCA 505 AAACAGGCTTTCTATTTTAGGTGTTGCGACGCACTACTTTACAGATGCTACTCAGCCA Gaps 787 GAAGCGCAGCGCGTTACAGCTGGTTATATTCATTTGTGGTTTGATACGTATGT 839 853 AAAGCGCAAAGAAACACGGCGGGATTTATTCATTTATGGTTTAAAACATATGT 905 APPLICANT: Hazlewood, Geoff
APPLICANT: Lam, David B.
APPLICANT: Lam, David B.
APPLICANT: Lam, David B.
APPLICANT: Lam, David B.
APPLICANT: Barton, Nelson B.
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM AND TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM CURRENT APPLICATION NUMBER: US/10/421,654
CURRENT FILING DATE: 2003-04-21
PRIOR PLICATION NUMBER: US 60/374,313
PRIOR PLILING DATE: 2002-04-19 18; Length 1422; Indela ; FEATURE: ; OTHER INFORMATION: Obtained from an environmental sample US-10-421-654-97 Score 85.8; DB 16; Pred. No. 2e-10; 0; Mismatches 232;

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724 TCTGAAGAATATGCAGATAAATGGCGTGGGAAGTAACACCGGTGACAGGAAAGCGTTTA 783
664 CAAGATTATCCTGGCGTTGTGAACGATACGACAAAAGATTGGTTTGTAAAAGCAGCCGTA 723
                                                                                                                                                                                                                                                               Sequence 81, Application US/10421654; Publication No. US20040005604A1; GENERAL INFORMATION: APPLICANT: Gramatikova, Svetlana
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                                                                                                                                                                                                                793 AAAGGAAACAATGCTCTTTGGCAGCAAGAGTTATGCCAGCTGTTCAGAGAAGTTTAGAA 852
                                             AATTGGAAAGGAGCAAACCCAGAAGATTGAATTGAAGGAGCAGCGGTAGCAGCTAAACAA 666
                                                                                                              667 GATTATCCTGGCGTTGTGAACGATACGACAAAAGATTGGTTTGTAAAAGCAGCCGTATCT 726
                                                                                                                                               739 GCAAAAGTGGAAATCGGGAACATTACCA-----ATGATGTGATTAAATCTCACTATAAT 792
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                                                                                                                                                                                                                                                                                                                                                               General Boy, Application US/10421654

| Saquence Boy, Application US/10421654
| Publication No. US200400056041|
| GENERAL INFORMATION:
| APPLICANT: Grammatikova, Svetlana | APPLICANT: Hazlewood, Geoff | APPLICANT: Hazlewood, Geoff | APPLICANT: Hazlewood, Geoff | APPLICANT: Barron, Nelson IR | TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM CURRENT APPLICATION NUMBER: US/10/421,654 | CURRENT PILING DATE: 2003-04-21 | PRIOR APPLICATION NUMBER: US 60/374,313 | PRIOR PILING DATE: 2002-04-19 | PRIOR PILING DATE: 2002-04-19 | PRIOR PILING DATE: PRESEQ ID NOS: 106 | SOFTWARE: PRESEQ FOR WINDOWS Version 4.0 | SEQ ID NO 89 | LENGTH 1422
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52.2%; Pred. No. 3.1e-08;
:ive 0; Mismatches 232;
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Matches 280; Conservative
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745 graciaaricagaacaftaccaardacaadarraaarcrcacrataaraadadaacaar
                                                        724 TCTCAAGAATATGCAGATAAATGGCGTGCGGAAGTAACACCGGTGACAGGAAAGCGTTTA
                                                                                                         805 gcrc-------rrrggcaacaagaagrrargccagcrgrccagagarrra
                                                                                                                                                                 784 ATGGAAGCGCAGCGCGTTACAGCTGGTTATATTCATTTGTGGTTTGATACGTATGT 839
                                                                                                                                                                                                Gaps
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8.5%; Score 72; DB 16; Length 1422;
Best Local Similarity 51.7%; Pred. No. 4.5e-07;
Matches 277; Conservative 0; Mismatches 235; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Obtained from an environmental sample US-10-421-654-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hallenger, Gooff
APPLICANT: Hallenger, Gooff
APPLICANT: Hallenger, Gooff
APPLICANT: Lam, David E.
APPLICANT: Lam, David E.
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENC
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENC
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENC
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC AND USING THE
FILE REFERENCE: 09010-094-01
CURRENT FILING DATE: 2003-04-19
NUMBER OF SEQ ID NOS: 106
SOFTHARE: PASLEEG for Windows Version 4.0
SEQ ID NO 81
LENGTH: 1422
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RESULT 13
US-10-329-624-470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 ATCGTGCAATTGACATCATGTCTCGTAATACAACGATTGTGAATCCGAATGAAACTGCAT 226
--TTTGGCAACAAGAAGTTATGCCAGCTGTCCAGAGGAGTTTA 849
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Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE ON INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5.255
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 AACTTAAAAATTTCGACAAACAAATTGCTCAAGGAATATATGACGCGGATCATAAAATC 48
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                                                                 850 GAGAACGCACAAAAAAAAACACGCGCGATTTATTCATTTATGCTTTAAAACATTTGT
                                  784 ATGGAAGCGCAGCGCGTTACAGCTGGTTATATTCATTTGTGGTTTGATACGTATGT
                                                                                                              RESULT 11
US-10-398-221-3772/c
Sequence 3772, Application US/10398221
Sequence 3772, Application US/10398221
Sequence 3772, Application US/10398221
GENERAL INFORMATION:
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
TITLE OF INVENTION: Listeria innocua, genome and applications
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR FILING DATE: 2003-01-10-04
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR APPLICATION NUMBER: FR 00/12 697
SPIOR APPLICATION NUMBER: PR 00/12 697
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: PatentIN Version 3.0
SEQ ID NO 3772
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Pred. No. 0.0029;
0; Mismatches 106; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
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Best Local Similarity 53.3%;
Matches 121; Conservative
805 GCTC----
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US-08-781-986A-470
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Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Pannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4223 TGATGGTCAGATTTCAGAAATGAAAGAAAGAAATTGAAAAGCTTGAAAATCAAAGACG 4282
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Pred. No. 11;
0; Mismatches 221; Indels
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MSDOS version 6.2
                      SOPTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
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Publication No. US20040043037A1
                                                                                                                                                                                                                                                          NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB246
TELECOMMUNICATION INPORMATION:
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 470:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Charles Kunsch
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                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9821 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 44.3
Matches 176; Conservative
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OPERATING SYSTEM:
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                                                                                                         FILING DATE
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700 cerradearereceaececearrearrirearearereceraraarricaeearri 641
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APPLICANT: QUINN, Cheryl
APPLICANT: ARVIDSON, Staffan
APPLICANT: ARVIDSON, Staffan
APPLICANT: HARRIS, Douglae
APPLICANT: HARRIS, Douglae
APPLICANT: MOTT, John
TITLE OF INVENTION: ANTIMICROBIAL METHODS AND MATERIALS
FILE REFERENCE: 00774.USI CN1
CURRENT APPLICATION NUMBER: US/10/429,094
CURRENT FILING DATE: 2003-05-02
PRIOR FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 145
SOOFWARE: Patentin version 3.0
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                                                                                 APPLICANT: MOTT, John
TITLE OF INVENTION: ANTIMICROBIAL METHODS AND MATERIALS
FILE REPRENCE: 6212.N2
CURRENT APPLICATION NUMBER: US/09/966,521
CURRENT FILIG DATE: 201-09-28
NUMBER OF SEQ ID NOS: 145
SOFTWARE: Patentin version 3.0
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 403 GGTCAAGCATACCAAAATCAAGATATGCAGCAAGCATTCT
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Pred. No. 3.4;
0; Mismatches 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 21, Application US/10429094; Publication No. US20030180821A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Staphylococcus aureus
US-09-966-521-21
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.1%;
Best Local Similarity 50.5%;
Matches 105; Conservative
                                      ARVIDSON, Staffan
HARRIS, Douglas
MOTT, John
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TOMICH, Che-Shen
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                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                     ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
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                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/329,624

FILING DATE: 27-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/956,171

FILING DATE: October 20, 1997

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248PID1
TELECOMMUNICATION INFORMATION:
TELEPHAR: (240) 314-1224
INFORMATION FOR SEQ ID NO: 470:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 470:
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) Sequence 21, Application US/09966521
) Publication No. US20030087321A1
) GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 9821 base pairs
LTMPE: nucleic acid
STRANDEDNESS: double
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Search completed: August 2, 2004, 04:20:53 Job time : 511 secs

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August Run on:

1, 2004, 23:39:34; Search time 432 Seconds (without alignments) 8348.889 Million cell updates/sec

PCT-US03-12556-1 849

Title: Perfect score:

1 atgaaaaagaaagtattagc.......8tacgtatgtaaatcgctaa 849 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 seqs, 2124099041 residues Searched:

Total number of hits satisfying chosen parameters:

6747726

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_29Jan04:* Database :

geneseqn2002s:* geneseqn2003as:* geneseqn2001as:* geneseqn2001bs:* geneseqn1990s:* geneseqn1980s:*

geneseqn2003bs:* geneseqn2003cs:* geneseqn20048:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Abq67927 Listeria	Abq69833 Listeria	Continuation (3 of	Abg70959 Listeria	Aat36392 Lactococc	Aav74781 Staphyloc	Aaa70152 Plasmodiu	Aaa70178 Plasmodiu	Ada71938 Rice gene	Acf72350 Staphyloc	Acf74582 Staphyloc	Adc21339 Staphyloc	Adc25025 DNA encod	Add52527 Staphyloc	Aaa70220 Plasmodiu	Aav74441 Staphyloc	Abk28258 DNA trans		Abq39490 Oligonucl			Abl92260 Chemicall	Aac84742 S. pneumo
ΩI	ABQ67927	ABQ69833	ABA03041_02	ABQ70959	AAT36392	AAV74781	AAA70152	AAA70178	ADA71938	ACF72350	ACF74582	ADC21339	ADC25025	ADD52527	AAA70220	AAV74441	ABK28258	AAA68254	ABQ39490	ABQ39491	ABL33586	ABL92260	AAC84742
% Query Match Length DB	870 6	870 6	9 00001	4562 6	3706 2	9821 2	6033 3	3738 3	2000 7	6222 7	837 7	837 9	837 9	837 9	2700 3	5924 2	8170 6	43095 3	9 696	9 696	6227 6	6227 6	2319 4
& Query Match Le	18.2	18.2	18.2 13	6.8	5.5	5.4	5.3	5.3	5.3	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	4.9	4.9	4.9	4.9	4.9
Score	154.4	154.4	154.4	57.4	46.6	45.8	45.4	45.2	45	43.4	43.2	43.2	43.2	43.2	43.2	43.2	43	43	42	42	41.8	41.8	41.6
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Aav52332 Streptoco	Abg77399 Human col	Aaz91806 Streptoco	Abx06302 S. pneumo	Aca49616 Prokaryot	Continuation (17 o	Abg67195 Listeria	Continuation (5 of	Continuation (6 of	Ada71938 Rice gene	Abl19460 Drosophil	Abq75107 Anopheles	Acf79720 Mosquito	Aaa70211 Plasmodiu	Aca43139 Prokaryot	Aas51736 Staphyloc	Aas54787 Staphyloc	Aaq62305 Clostridi	Aax99537 Nucleic a	Aca52696 Prokaryot	Aaq10244 Streptoco	Aat49317 Type-6 M-
AAV52332	ABQ77399	AAZ91806	ABX06302	ACA49616	ABQ69245_16	ABQ67195_0	ABS56454 04	ABS56454 05	ADA71938	ABL19460	ABQ75107	ACF79720	AAA70211	ACA43139	AAS51736	AAS54787	AAQ62305	AAX99537	ACA52696	AAQ10244	AAT49317
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ALIGNMENTS

ABQ67927 standard; DNA; 870 BP. (revised)
(first entry) 29-AUG-2003 29-AUG-2002 ABQ67927; RESULT 1 ABQ67927

Listeria monocytogenes EGD DNA sequence #51

Antibacterial; Listeria; food contamination; mutational analysis; infection; ds.

Listeria monocytogenes; EGD.

WO200228891-A2:

11-APR-2002.

04-OCT-2001; 2001WO-FR003061.

04-OCT-2000; 2000FR-00012697.

(INSP) INST PASTEUR. (CNRS) CNRS CENT NAT RECH SCI.

Kunst F, Glaser P;

WPI; 2002-332479/37.

New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators.

Claim 16; SEQ ID NO 740; 180pp; French.

The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines. Note: The sequence data for this patent did not form

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Arcaagcaacggaagacarggragcaaaagarrrrgcrcagargacgraaagacrggc 679
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part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                   CACCGATTTTAAGATGGTCAGCTGAGGATAAGCATAATGAGGGGATTAACTCTCATTTGT
                                                                                                                       CACATAAACTTAGTTGGTCCGCGGTAACCCGACAAATACTGACGTAAATACGCACTATT
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                                                              DB 6; Length 870;
                                         Sequence 870 BP; 328 A; 149 C; 160 G; 233 T; 0 U; 0 Other;
                                                           Query Match
18.2%; Score 154.4; DB 6; Length
Best Local Similarity 53.1%; Pred. No. 3.9e-29;
Matches 329; Conservative 0; Mismatches 291; Indels
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(first entry)
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The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in antilisteria vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                               New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators.
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Pred. No. 3.9e-29;
0; Mismatches 291; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 16; SEQ ID NO 2646; 180pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 18.2%;
Best Local Similarity 53.1%;
Matches 329; Conservative C
04-OCT-2001; 2001WO-FR003061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic aspens) also for treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/publpublished_pot_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                           TTGAAGGAGCAGCGGTAGCAGCTAAACAAGATTATCCTGGCGTTGTGAACGATACGACAA
                                                                                                                                                                         ATATTGTTTCAGATAGGATATTGGAATTGGAAAGGAGCAAACCCAGAAGATTGGA
  CTTATCCAATGGGTTTCCATTCTAAATACGAAAATTTTGTTGATACAATAAAAATAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Listeria monocytogenes 4b contig DNA sequence #901.
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(CNRS ) CNRS CENT NAT RECH SCI
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                                                                                              166
                                                                                                                                   227 TIAGITGGICCGCGGATAAICCGACAAATACTGACGIAAATACGCACTATIGGCTITITA 168
                                                                                                                                                                       ATCGTGCAATTGACATCATGTCTCGTAATACAACGATTGTGAATCCGAATGAAACTGCAT 226
                                                                                                                                                                                                           107 AACTIAAAAATITCGACAAACAAATIGCICAAGGAATATATGACGCGGATCATAAAATC 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactococcus lactis subsp. cremoris W9 restriction-modification system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lactic acid bacterium; Danish starter culture; cheese; enzyme;
restriction endonuclease; methylase; fermented milk; phage resistance;
                                                                                            TAAGATGGTCAGCTGAGGATAAGCATAATGAGGGGATTAACTCTCATTTGTGGATTGTAA
                                                          Gaps
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                Length 4562;
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/*teg= b
/codon_grart= 2464
/product= "Liabl restriction endonuclease"
/evidence= EXPERIMENTAL
                                                                                                                                                                                                                                                                                                                                                                caratrardaracradracerritrarcricarritrararccrdar 1
                Score 57.4; DB 6; Length 4 Pred. No. 0.00024; 0; Mismatches 106; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "LlaBI methylase"
/evidence= EXPERIMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactococcus lactis subsp. cremoris; W9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
complement (422. .2161)
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AAT36392 standard, DNA; 3706
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                    6.8%;
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                                      al Similarity 53.3
121, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (JOSE/) JOSEPHSEN J.
(NYEN/) NYENGAARD N.R.
(VOGE/) VOGENSEN F.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MADS/) MADSEN A.
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08-DEC-1996
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                    Query Match
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                                                                                                                                                                                                                                   This DNA encodes the plasmid-derived type-II restriction- modification system from Lactococcus lactis subsp. cremoris W9, Liabl, and contains 2 of the transcribed in the same direction and coding for putative proteins of 580 AA (Liabl methylase M.Liabl; AAM02164) and 299 AA (Liabl endonuclease R.Liabl; AAM02165). This restriction-modification system may be used in a method for conferring increased virus resistance, more specifically phage resistance, to a L. lactis strain used in cheese manufacture. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 AGTICAAAGIGIAGIAITIGCACAAACAAATAATAGIGAAAGICCIGCACCGAITITAAG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 TGCAATTGACATCATGTCTCGTAATACAACGATTGTGAATCCGAATGAAACTGCATTATT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 AAATGAGTGGCGTGCTGATTTAGAAAATGGTATTTATTCTGCTGATTACGAGAATCCTTA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1010 ATTIBATCGARTARIATATCCTTATGARARIATGARCGGCARTGCTGTACCARTCATCAGCAT 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       890 gcrcagraagccaargcrccaaaaccaaccarraacarrrgcrardaararcgccaarc 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                830 TCAAGCATTGAATAGCCATGTACCTAAAATAATTTTCCTACAAATTCTTTGAATCCAAA 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a //note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2811. .2880
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Type II restriction-modification systems obtd. from Lactococcus lactis for conferring phage resistance on lactic acid bacteria, useful as starter cultures for cheese and fermented milk prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 ATGGTCAGCTGAGGATAAGCATAATGAGGGGATTAACTCTCATTTGTGGATTGTAAATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  950 TGTCTCAATGAAGGAAAATTCCCTAATACTTTAAATTATTTTATTGCTATTAAAGACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.5%; Score 46.6; DB 2; Length 3706; 47.7%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3706 BP; 1284 A; 535 C; 575 G; 1312 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 TTATGATAATAGTACATATGCTTCTCACTTTTATGATCCGGATAC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  770 CITIGIALATITIACAGAITAIGCICITITITAATAAIGGATAIGC 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus contig SEQ ID #470.
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                                                                                                                                                                     Claim 2; Page 67-69; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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1283 TGACATCACTGTTAAAGAATTGAGTAAGACTGAAAAAGAGCAAGAGCGTATTTAGTAAG 4342

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of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM: Homology searches using the S.aureus DNA sequences allows puttative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can be used for including cellulities are useful as primers or probes for isolating characterisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        any of the S.aureus DNA sequences contained on the computer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence represents one of 5191 Staphylococcus aureus DNA sequences
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/note= "these bases represent a line of missing text in
/note= "these bases represent a line of missing text in
the sequence listing in the specification. They are
included to maintain the nucleotide numbering given in
the specification for this DNA sequence"
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the sequence listing in the specification. They are
included to maintain the nucleotide numbering given in
the specification for this DNA sequence"
                     4621. .4680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus - in the production of anti-
the sequence listing in the specification. They are included to maintain the nucleotide numbering given the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9821 BP; 3652 A; 1311 C; 1978 G; 2575 T; 0 U; 305 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.4%; Score 45.8; DB 2; Length 9821; 38.8%; Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fannon MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     otide(s) and proteins derived from computer readable medium and used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 1387-1392; 3271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97EP-00100117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0009861P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotide(s) and stored on computer rea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-374922/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S.aureus vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           readable medium
                                                         misc_feature
                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JAN-1997;
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                                                                                                                                                                                                                       4523 TGATCAAAGACATAAGGATGAAGTAAGAAAGGCAAAATCTAAAAAAGATGCTGTAGTAGA 4582
                               4343 AATGCAAAGAAACAGAAATGCTTATTCAATAGACGAAGCGAGCAAAGCAATTAAAGAAGC 4402
                                                                                                                                                                                                                                                                                  The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II). (I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisers or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they
                                                                                                                                                                                       680
                                                                                                                                                                                                                                                    TGTGAACGATACGACAAAAGATTGGTTTGTAAAAGCAGCCGTATCTCAAGAATATGCAGA 740
                                                              AAACTITACGAATCTTTCTTATCCAATGGGTTTCCATTCTAAATACGAAAATTTTGTTGA
                                                                                          <u> Agaaaagcaaggaaagcaagaaaaaaaaagaagrggaraagcagrargaagargargrcar</u>
                                                                                                                                                                                       621 AAACCCAGAAGATTGGATTGAAGGAGCAGCGGTAGCAGCTAAACAAGATTATCCTGGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:285.
                                                                                                                           TACAATAAAAATAACTATATTGTTTCAGATAGCAATGGATATTGGAAATTGGAAAGGAGC
                                                                                                                                                        4463 TGCTATAAAAATAACGTCAACCTTTCTAAGTCTGAAAAAGATAAATTGTTAGCTATTGC
   Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            parasite,
and in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteins encoded by chromosome 2 of the human Plasmodium falciparum, useful as antimalarial diagnosis of P.falciparum infection.
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CARUCCI D.
GARDNER M.
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0; Mismatches 282; Indels

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Similarity

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1223 TGATGGTCAGATTTCAGAAAATGAAAGAAAAGAAATTGAAAAGCTTGAAAATCAAAGACG 4282 TTATGATCCGGATACTGGAACAACATATATTCCTTTTGCGAAACATGCAAAAGAAACAGG 380

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5042 AIAATATTTTTTATGATAATCATGATACCAATAATAATAATAATAATAATAATAATAATAATA
 are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5102 ATAATAATAATAATAATAATAATAATAATATATATGTCTTAAGAATAATAAAAATAATA 5161
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                                                                                                                                                                                                                                                      Sequence 6033 BP; 3019 A; 437 C; 707 G; 1870 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                             Query Match
5.3%; Score 45.4; DB 3; Length 6033;
Best Local Similarity 45.2%; Pred. No. 0.29;
Matches 166; Conservative 0; Mismatches 201; Indels 0
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antimalarial; malaria;
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II). (I) and polyclonal antisers or a monoclonal antibody raised to infection. (I) and polyclonal antisers or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of infection with P. falciparum infection, or they can be used to identify drug resistance in P. falciparum infection, or they can be used to identify drug resistance in P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the confoction of proteins concoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2730 TAAGACAATGGAAAATAAACCGAACTTAACAAATAAAATTATATGAATAATGACAATAT 2789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant; bacterial infection; fungal infection; viral infection; rice;
                                                                                                                                                                        Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection.
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                                                                                        Venter JC;
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                                                                                      Gardner M,
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(CARU/) CARUCCI D. (GARD/) GARDNER M. (VENT/) VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification
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                                                                                    Hoffman S,
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                                                                                                                                                                                                                              The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                             844 RARKARYWWKWATWCATKRWMTKGKGAKWAWTWMAKAWRKYYWSWMRAWYYYYKTRRTRY
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11arity 11.2%; Pred. No. 0.26;
Conservative 166; Mismatches 131; Indels
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                                                                                                           J, Goff
Xie Z,
                                                                                                           Glazebrook
Whitham S,
                                                                                                                                                                                                              Claim 27; SEQ ID NO 5263; 899pp; English.
                                                                                        (SYGN ) SYNGENTA PARTICIPATIONS AG
                                                22-JUN-2001; 2001WO-IB001105
                                                                    22-JUN-2001; 2001WO-IB001105
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         WO2003000898-A1.
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Katagiri
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3330 IGCTATAAAAATAACGTCAACCTTTCTAAGTCTGAAAAGATAAATTGTTAGCTATTGC 3389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rcarcacarrrcacaaaarcaaaacaaaacaarrcaaaagcrrcaaaarrcaaagacc 3149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTATGATCCGGATACTGGAACAACATATATTCCTTTTGCGAAACATGCAAAAGAAACAGG 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein, useful as a vaccine for treating or infection, specifically an infection caused
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                                                         Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis; enzymatic assay; antibiotic target; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 6222;
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Staphylococcus aureus DNA #30
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preventing Staphylococcal
S. aureus, e.g. sepsis.
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                                                                                                                                                 Staphylococcus aureus
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The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nutileic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus genes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403 GGTCAAGCATACCAAAATCAAGATATGCAGCAAGCATTCTTCTACTTAGGATTATCGCTT 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   760 AATTATTCACATGAAAAGCTTCATTAAAAACTTTCTTCAATTATGAACATATTCAATGA 701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused by S. aureus, e.g. sepsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 837 BP, 314 A; 116 C; 149 G; 258 T; 0 U; 0 Other;
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                                                                                                                                    Staphylococcus aureus DNA #2262.
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                  .582/c
ACF74582 standard; DNA; 837 BP.
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                                                                                                                                                                                                                        Staphylococcus aureus
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P-PSDB; ABM73022.
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The invention relates to methods of identifying an agent that binds a polypeptide from Staphylococcus aureus by contacting a polypeptide and an agent to form a mixture and determining whether the agent binds the polypeptide. The method is useful in identifying agents that bind gene products critical for the survival of microbes, preferably staphylococcus microbes, including agents that interfere with the function of such groducts. The method is used to identify new agents useful for treating products. The method is used to identify new agents useful for treating or preventing bacterial infections, particularly those caused by antibiotic-resistant bacteria. This sequence represents the coding region for a protein from Staphylococcus aureus of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      463 CATTATTAGGAGATGTGAATCAGCCAATGCATGCAGCAACTTTACGAATCTTTAT 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying an agent that binds a polypeptide and useful for treating or preventing staphylococcal infections, comprises contacting a polypeptide and an agent to form a mixture and determining whether the agent binds the polypeptide.
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                                                                                                     Staphylococcus aureus protein coding sequence SEQ ID NO: 21.
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5.1%; Score 43.2; DB 9; Length 837;
Best Local Similarity 50.5%; Pred. No. 0.58;
Matches 105; Conservative 0; Mismatches 103; Indels (
                                                                                                                                        ds; gene; antibacterial; gene therapy; vaccine; diagnosis; microbial survival; gene function; bacterial infection; antibiotic-resistant bacterium.
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1..837
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   DNA; 837 BP.
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                                                                                                                                                                                                              Staphylococcus aureus.
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 ADC21339 standard;
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                                   ADC21339;
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The invention discloses a method for identifying an agent that binds a polypeptide which comprises mixing a polypeptide and an agent to form a mixture and determining whether the agent binds the polypeptide. Also claimed is a method for identifying an agent that decreases the growth rate of a microbe, making a Staphylococcus aureus with reduced virulence, which comprises altering a coding sequence in an S. aureus to introduce a mutation, a vaccine composition comprising the S. aureus organism with reduced virulence. The methods are useful for identifying an agent that ceduced virulence. The methods are useful for identifying an agent that infections, particularly those caused by antibiotic-resistant bacterial infections, particularly bacteraemia, septic shock and serious metastatic infections of including endocarditis, arthritis, osteomyelitis, pneumonia, abscesses in virtually any organ, skin rashes, food poisoning or multisystem dysfunction, i.e. toxic shock syndrome. The inventive method identifies agents that are unrelated to existing antimicrobials and that target different aspects of staphylococcal invasion of and replication in the host. The sequence presented is a DNA sequence encoding one of the S. aureus polypeptides of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identification of agent that binds polypeptide, for treating bacterial infections, particularly caused by antibiotic-resistant bacteria, involves mixing polypeptide and agent, and determining whether agent binds polypeptide.
                                                                                                                                                  Binding agent; growth rate; microbe; virulence; vaccine; bacterial infection; antibiotic-resistant bacteria; bacteraemia; septic shock; metastatic infection; endocarditis; arthritis; osteomyelitis; pneumonia; abscess; skin rash; food poisoning; multisystem dysfunction; toxic shock syndrome; antimicrobial; antibacterial; immunosuppressive; cytostatic; antiinflammatory; gene;
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                                                                                                                S. aureus polypeptide #11.
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ADC25025 standard; DNA; 837 BP.
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                                                                         (first entry)
                                                                                                                                                                                                                                                                                           Staphylococcus aureus
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ARVIDSON S.
MOTT J E.
HARRIS D W.
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                                                                                                             DNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus, microbe survival; infection; antibiotic-resistant bacteria; critical coding sequence; essential coding sequence; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus unknown coding region #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mott JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.58;
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                                                                                                                                                                                                                                           583 GTTTCAGATAGCAATGGATATTGGAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleocide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II). (I) and polyclonal antibody raised to infection. (I) and polyclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are risins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum. Sequencing of the confluence or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the confluence of prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the confluence of managered by the complexity of the parasitic lifecycle, and process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB1814 to AAB18352 cepresent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the
                                      641
   COTTAGCATGTGCGACACCAATGGATTTGATTTCATGATCTCCTATAAATTCAGCAATTT
                                                                                                                                                                                                                                                                                       Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:353
                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum, chromosome 2; human malaria parasite; vaccine, antimalarial; malaria; protozoacide; infection; insecticide; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection.
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                                                                                         640 CCITTITCAAGIAITGGATACTAGAAIT 613
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                                                                                                                                                                                     AAA70220 standard; DNA; 2700 BP
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CARUCCI D.
GARDNER M.
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Query Match 5.1%; Score 43.2; DB 3; 18est Local Similarity 47.2%; Pred. No. 0.82; Matches 200; Conservative 0; Mismatches 218;
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Sequence 9, Appli
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Sequence 1, 7
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*
(cgn2_6/ptodata/2/ina/5B_COMB.seq:*
(cgn2_6/ptodata/2/ina/6A_COMB.seq:*
(cgn2_6/ptodata/2/ina/6B_COMB.seq:*
(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-956-171E-130
US-09-54-171E-130
US-08-961-527-199
US-08-31-538A-1
US-08-601-198-37
US-09-601-198-37
US-09-601-198-37
US-09-51-098-1
US-09-961-083-67
US-08-961-083-67
US-08-961-083-67
US-08-950-182-2
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5-09-218-207-73
5-09-338-907-183
5-09-218-207-183
5-09-976-594-125
3-09-134-001C-973
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                                                                                                                                                                                             682709 segs, 277475446 residues
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                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                  nucleic search, using sw model
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                                                                                                                                                                                                                                       seq length: 0
seq length: 200000000
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Match Length
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10207
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15766
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37950
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Maximum DB
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Sequence 2813, Ap
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Sequence 5, Appli
Sequence 2404, App
Sequence 120, App
Sequence 120, App
Sequence 1179, Ap
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ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: Poley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITT: Alexandria
STATE: VA
                                                                          US-09-601-198-178

US-09-134-001C-1835

US-08-914-479A-3

US-08-914-479A-5

US-08-914-479A-5

US-08-95-475-5

US-08-95-475-5

US-08-95-171E-200

US-08-95-171E-200

US-08-95-171E-200

US-08-915-171E-200

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US-09-888-655-1
US-09-134-001C-1054
US-08-11-434A-2
US-09-762-724-3
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
APPLICATION NUMBER: US/07/935,313
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENTY Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (703)836-9300
TELEFAX: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-232-463-14/c
; Sequence 14, Application US/08232463
Patent No. 5670367
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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579
655
858
1332
1617
4554
7172
7172
1664976
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STRANDEDNESS: single
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OTHER INFORMATION:
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TITLE OF INVENTION: restriction-modification systems from Lactococcus lactis
NUMBER OF SEQUENCES: 14

NUMBER OF SEQUENCES: 14

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,159
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                                                                                                                                                                                                             541 AAATACGAAAATTTTGTTGATACAATAAAAATAACTATATTGTTTCAGATAGCAATGGA 600
                                                                                                                      601 TATTGGAATTGGAAAGGAGCAAACCCAGAAGATTGGATTGAAGGAGCAGCGGTAGCAGCT 660
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                                                                                                                                                                                                                                                            721 GTATCTCAAGAATATGCAGATAAATGGCGTGCGGAAGTAACACCGGTGACAGGAAAGCGT
                     Gaps
                     ö
                   Indels
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: /product= "LlaBI endonuclease"
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/codon_start= 422
/product= "LlaBI methylase"
/evidence= EXPERIMENTAL
/gene= "RR"
Best Local Similarity 4.7%; Pred. No. 0.0033; Matches 12; Conservative 151; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
ORGANISM: Lactococcus lactis subsp. cremoris
STRAIN: WS6
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PRICH APPLICATION DATA:
PRICH APPLICATION DATA:
APPLICATION NUMBER: DK 0179/95
FILING DATE: 17-FEB-1995
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3706 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Patent No. 6300109
GENERAL INFORMATION:
APPLICANT:
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DENTIFICATION METHOD:
OTHER INFORMATION: /cod
OTHER INFORMATION: /prod
OTHER INFORMATION: /evi
OTHER INFORMATION: /gen
OTHER INFORMATION: /stan
OTHER INFORMATION: /stan
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IDENTIFICATION METHOD:
OTHER INFORMATION: /co
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NAME/KEY:
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Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TILLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 2556
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                        111 ATGGTCAGCTGAGGATAAAGCATAATGAGGGGATTAACTCTCATTTTGTGGATTTGTAAATCG 170
                                                                                                                                                                                                                                                                                                                                                        1010 ATTTAATCGAATAATATATCCTTATGAAATATGAACGGCAATGCTGTACCAATCAGCAT 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 IGCAATTGACATCATGTCTCGTAATACAACGATTGTGAATCCGAATGAAACTGCATTATT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   890 GCTCAGTAAACGCAATGCTGGGAAACCAACCGTTAACATTTGGTATGAATATGGGCGATC 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 AAATGAGTGGCGTGCTGATTTAGAAAATGGTATTTATTCTGCTGATTACGAGAATCCTTA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   830 TCAAGCATTGAATAGCCATGTACCTAAAATAATTTTTCCTACAAATTCTTTGAATCCAAA 771
                                                                                                                                                                                                                                                                                                     51 AGTTCAAAGTGTAGTATTTGCACAAACAAATAATAGTGAAAGTCCTGCACCGATTTTAAG
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                   Score 46.6; DB 4; Length 3706;
Pred. No. 0.0041;
0; Mismatches 149; Indels 0
                                                                          "Gene coding for LlaBI
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HD Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
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APPLICATION UNDERS: US/08/956,171E
FILING DATE: 20-0ct-1997
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/09,861
FILING DATE: January 5, 1996
APPLICATION UNDERS: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
/evidence= EXPERIMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Human Genome Sciences, STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
                                                                          standard name=
                                                                                                                             /label= r-llaBI
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; Sequence 470, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
                                                                                                        endonuclease"
                     /gene= "ORF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gil H. Choi
Patrick S. Dillon
                                                  'number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Charles Kunsch
Gil H. Choi
                                                                                                                                                                                                     5.5%;
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STATE: Maryland
COUNTRY: USA
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OTHER INFORMATION:
                     INFORMATION:
INFORMATION:
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Craig A. Rosen
Steven C. Barash
Michael R. Pannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4522
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                                                                                                                                                                                                                                                                                       TGATGGTCAGATTTCAGAAAATGAAAAAAAAAATTGAAAAGCTTGAAAATCAAAGACG 4282
                                                                                                                                                                                                                                                                                                                                                             4283 TGACATCACTGTTAAAGAATTGAGTAAGACTGAAAAAGAGCAAGAGCGTATTTTAGTAAG 4342
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                                                                                                                                                                                                                                                     321 TTATGATCCGGATACTGGAACAACATATTTCCTTTTGCGAAACATGCAAAAGAAACAGG 380
                                                                                                                                                                                                                                                                                                                           AAACTITIACGAATCITITCITATCCAATGGGTTTCCATTCTAAATACGAAAATTTTGTTGA 560
                                                                                                                                                                                                                                                                                                                                                                                                  TACAATAAAAATAACTATATTGTTTCAGATAGCAATGGATATTGGAATTGGAAAGGAGC
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                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                            Score 43.4; DB 4; Length 9821;
Pred. No. 0.046;
0; Mismatches 221; Indels 0
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COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4583 CGTTGTTAAAAGCAAAATAAAGATATTGATAAAGAA 4619
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APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: CURROWN>
                                                                                               TOPOLOGY: linear
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SEQUENCE DESCRIPTION: SEQ ID NO: 470:
US-08-956-171E-470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-08-956-171E-130/c
Sequence 130, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
GILH. Choi
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 470:
SEQUENCE CHARACTERISTICS:
LENGTH: 9821 base pairs
                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                              Query Match 5.1%;
Best Local Similarity 44.3%;
Matches 176; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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APPLICANT: GARY BRETON
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL.
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
PRIOR FILING DATE: 2000-04-05
PRIOR PLING DATE: 1999-04-09
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Pred. No. 0.057;
0; Mismatches 135; Indels
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50.5%; Pred. No. 0.043;
iive 0; Mismatches 103;
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                                                                ATTORNEY/AGENT INPORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PE248P1
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 130:
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
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                                                                                                                                                                                         TELEPHONE: (240) 314-1224
                                                                                                                                                                                                          FELEFAX: (301) 309-8439
                                                                                                                                                                                                                                                                                    LENGTH: 5924 base pairs
                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 47.7
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 50.5
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 455
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                                                                                                                                                                                                                                                                                                                                                                                                          US-08-956-171E-130
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284 ATAAACCTACTTTTGATGTATCGAAAAAGGAAAGATAACCCACAAGTAAACCATAGTCAAT 343
                                                                                                 452 GAITAICGCTICAITAITTAGGAGAIGIGAAICAGCCAAIGCAIGCAGCAAACTITACGA 511
                                                                                                                                                     344 TAAATGAAAAGICACAGAAAAGGATTTACAAAGAAGAAGAACATTCACAAAAATCTGATT 403
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                                                                                                                                                                                                                                                               404 caaciaaggaigtrakggciacagricrigaraaaakaaiaigagagagagaaardakga 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08341538A
Fatent No. 5817317
GRNEAL NO. 5817317
GRAPEL AND FORMATION:
APPLICANT: TITBALL DR, RICHARD W
APPLICANT: WILLIAMSON DR, ETHEL D
TITLE OP INVENTION:
CLOSTRIDIUM PERFRINGENS VACCINES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
FILING DATE: US/08/341,538A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: NIXON & VANDERHYE
STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
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PRIOR APPLICATION DATA;
APPLICATION NUMBER: 68 9210717.6
FILING DATE: 20-MAY-1992
PRIOR APPLICATION NUMBER: 28-MIN-1992
PRIOR APPLICATION NUMBER: 28-JUL-1992
PRIOR APPLICATION NUMBER: 28-JUL-1992
PRIOR APPLICATION NUMBER: 20-MAY-1993
ATTORNEY/AGRET INFORMATION:
NAME: CRAWFORD, ARTHUR R
REGISTRATION NUMBER: 25327
INPORMATION FOR SEG ID NO: 1: SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: BIT PLOOR, 1100 NORTH GLEEN STREET: BIT PLOOR, 1100 NORTH GLEEN STATE: VINGINIA STATE: STREET: BIT STATES STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STRE
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ORIGINAL SOURCE:
CRISTNAL SOURCE:
CLOSTRIGHUM perfringens
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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TYPE: nucleic acid
GTRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                         572 ATAACTAT 579
                                                                                                                                                                                                                                                                                                                                                                               464 CTAACAAT 471
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736..1110
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CLASSIFICATION:
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NAME/KEY:
LOCATION:
FEATURE:
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; LOCATION:
US-08-341-538A-1
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Patent No. 6420135
GENERAL INFORMATION:
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                      1732 GATGATAATGGTGAGTATTCCGATACACTGCCTTTATCTCCAGATGATTTTAAGAAAAT 1791
                                                                                                                                                                    1792 Grcitaacigaagaataaaaahdirgcccarcaatgaaagaagaagtatttaaacag 1851
530 GTTTCCATTCTAAATACGAAAATTTTGTTGATACAATAAAAATAACTATATGTTGTTCAG 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 ATACTGGAACAACATATTCCTTTTGCGAAACATGCAAAAGAAACAGGCGCAAAATATT 391
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4.9%; Score 41.6; DB 4; Length 2911;
Bast Local Similarity 44.6%; Pred. No. 0.088;
Matches 164; Conservative 0; Mismatches 204; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20850

CIP: 20850

MEDIUM TYPE: Diskette, 3.50 inch, 1.4MD storage COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII Text
CURBLY APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
FLING DATE:
REASIFICATION: 424
APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                              1852 TTAATAAGAGAAAATAGA 1869
                                                                                                                                                                                                                              590 ATAGCAATGGATATTGGA 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maryland
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U8-08-961-527-199
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STATE: M
COUNTRY:
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MOLECULE TYPE:
                                                                                     ORGANISM:
                                                                                                                                                                                                                                               ; LOCATION:
US-08-725-518-1
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                                                                                                                                                                                                                                                                                                                                                            Matches 125;
                                                                                                               STRAIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                    FEATURE:
                                                                                                                                    FEATURE:
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                                                                                     243 TGCTGATTTAGAAAATGGTATTTATTCTGCTGATTACGAGAATCCTTATTATGATAATAG 302
                                                                                                                                156 ractrarccadarrardaraagaargcarardarcrararcaagarcarrrcroggarcc 215
                                                                                                                                                                               303 TACATATGCTTCTCACTTTTATGATCCGGATACTGGAACAACATATATTCCTTTTGCGAA 362
                                                                                                                                                                                                                          216 TGATACAGATAATAATTTCTCAAAGGATAATAGTTGGTATTTAGCTTATTCTATACCTGA 275
                                                                                                                                                                                                                                                                       363 ACATGCAAAAGAAACAGGGGCAAAATATTTTAACCTTGCTGGTCAAGCATACCAAAATCA 422
                                                                                                                                                                                                                                                                                                                 276 CACAGGGGAATCACAAATAAGAAAATTTTCAGCATTAGCTAGATATGAATGGCAAAGAGG 335
                                                                                                                                                                                                                                                                                                                                                                                             423 AGATATGCAGCAAGCATTCTTCTACTTAGGATTATCGCTTCATTATTAGGAGATGTGAA
4.7%; Score 39.8; DB 1; Length 1113;
46.8%; Pred. No. 0.18;
tive 0; Mismatches 142; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: TITBALL DR, RICHARD W
APPLICANT: TITBALL DR, ETHEL D
TITLE OF INVENTION: CLOSTRIDIUM PERFRINGENS VACCINES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTESTONDENCE ADUNESS:
ADDRESSER: NIXON & VANDERHYE
STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: UNITED STATES
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,518
FILING DATE: 4-OCT-96
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/341538
FILING DATE: 28-NOV-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: GB 9210717.6
FILING DATE: 20-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9215655.3
FILING DATE: 23-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO GB93/01039
FILING DATE: 23-JUL-1992
PRIOR APPLICATION NUMBER: WO GB93/01039
FILING DATE: 20-MAY-1993
ATYONER'AGENT INPORMATION:
APPLICATION NUMBER: WO GB93/01039
FILING DATE: 20-MAY-1993
ATYONER'AGENT INPORMATION:
ANAME. ANAMER. ADALTHING DATE: 20-MAY-1993
ATYONER'AGENT INPORMATION:
ANAME. ANAMER. ADALTHING DATE: 20-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                         483 TCAGCCAATGCATGCAGCAAACTTTAC 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 TACTCCATATCATCCTGCTAATGTTAC 422
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REGISTRATION NUMBER: 25327
REFERENCE/DOCKET NUMBER: 1:
INFORMATION FOR SEQ ID NO: 1:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
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                     al Similarity 46.8
125; Conservative
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US-08-725-518-1
  Query Match
                          Best Local
Matches 12
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243 TGCTGATTTAGAAAATGGTATTTATTCTGCTGATTACGAGAATCCTTATTATGATAATAG 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 CACAGGGGAATCACAAATAAGAAATTTTCAGCATTAGCTAGATATGAATGGCAAAGAGG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423 AGATATGCAGCAAGCATTCTTCTACTTAGGATTATCGCTTCATTATTTAGGAGATGTGAA 482
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4.7%; Score 39.8; DB 4; Length 1353;
Best Local Similarity 43.8%; Pred. No. 0.2;
Matches 173; Conservative 0; Mismatches 222; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                     Length 1113;
                                                                                                                                                                                                                                                                                                                                                                  Score 39.8; DB 2; Length 1
Pred. No. 0.18;
0; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cassell, Gail H.
APPLICANT: Cassell, Gail H.
APPLICANT: Chen, Ellson Y.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
CURRENT APPLICATION NUMBER: 1996/601,198
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/073,189
PRIOR FILING DATE: 1998-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    483 TCAGCCAATGCATGCAGCAAACTTTAC 509
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                                                                                                       : Clostridium perfringens
double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 37, Application US/09601198; Patent No. 6531583
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US-09-601-198-37
DNA (genomic)
NO
                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.7%;
Best Local Similarity 46.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 181
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                             CDS
736..1110
                                                                                                                                                                                  CDS
1..1110
                                                    ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-601-198-37/C
                              HYPOTHETICAL:
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LOCATION:
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581585 TAAAATTTTTTTTTTTAATTTAATGACGAGAAATAATAAGAGAGTTAATATTTAATATAT 581526
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                         581645 İGAALCATCGAAFTATTTİCAATACGAATAFTATİTTICAAAİTGTACGATGTAAAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 AGAAAATGGTATITATICTGCTGATTACGAGAATCCTTATTATGATAATAGTACATATGC
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                                                                                                                                                 Sequence 1, Application US/09790988

Patent No. 6632935

GENERAL INFORMATION

APPLICANT: SHIGENOBU, SHUJI

APPLICANT: MANABE, HIDEMI

APPLICANT: MANABE, HIDEMI

APPLICANT: MANABE, HIDEMI

TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS

FILE REFERENCE: 081356/0159

CURRENT APPLICATION NUMBER: US/09/790,988

CURRENT FILING DATE: 2001-02-23

PRIOR APPLICATION NUMBER: UP2000-107160

PRIOR FILING DATE: 2001-04-07

NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 640681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 4; Le
Pred. No. 4.1;
0; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          581465 TTTAACATGTATAATTTCATTTTACAT 581439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4M
COMPUTER: HP Vectra 486,33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 67, Application US/08961083; Patent No. 6159469; GENERAL INFORMATION: APPLICANT: Chol et. al. TITLE OF INVENTION: Streptococcus p. NUMBER OF SEQUENCES: 452; CORRESPONDENCE ADDRESS: ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.6%;
Best Local Similarity 49.3%;
Matches 102; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Buchnera sp.
                                                                                                          RESULT 11
US-09-790-988-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 640681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20850
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                                              62
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                                                                                   157 IGGAȚIGȚAAAICGIGCAATIGACAICAIGICTCGIAAIACAACGAITGIGAAICCGAAT 216
97 GCACCGAITITAAGAIGGICAGCIGAGGAIAAGCAIAAIGAGGGGAITAACICICAITIG 156
                                                            667
                                                                                                                                               607
                                                                                                                                                                         606 AAAACAATTCCACTAACACATATTCGCTCAATTTTAACTGCTTCATCAATTCCTTTAAA 547
                                                                                                                                                                                                                                                          277 TACGAGAATCCTTATTATGATAATAGTACATATGCTTCTCACTTTTATGATCCGGATACT 336
                                                                                                                                                                                                                                                                                                        546 AÁTAÁTGÁAAATTÁÍGÁTTTTTÁÍÁAAÁATAGÍTTÍAGTCÁTTTATÁTÁTGGÍGCTGGÍCAT 487
                                                                                                                                                                                                                                                                                                                                               486 ttägattttaäaägagcaatagaagcatataaääacgcaäaäcaaacaaaattttaacg 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285 TCCTTATTATGATAATAGTACATATGCTTCTCACTTTTATGATCCGGATACTGGAACAAC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 AIATATTCCTTTTGCGAAACATGCAAAAGAAACAGGCGCAAAATATTTTAACCTTGCTGG 404
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                                         726 acaaaotritatraaaaaaaaadgagataaaaatataaatrotaggaagatatrititotggg
                                                                                                                          866 cciatifgicaciggidgigatifactarigcaarcitatragatagataarakggtaar
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4.6%; Score 39.2; DB 4; Length 8:
Best Local Similarity 13.6%; Pred. No. 0.24;
Matches 49; Conservative 165; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
ITILE OF INVENTION: ESPS and Encoded Human Proteins.
FILE REPERENCE: GENSET, 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT RILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
                                                                                                                                                                                                                                                                                                                                                                                                                                     397 CTIGCIGGICAAGCAIACCAAAAICAAGAIAIGCA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426 AAACACAAAGATAAACAACTAGTTAAAGAAATGGA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2813, Application US/09621976 Patent No. 653963 Patent No. 643963 APPLICANT: INFORMATION: APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813
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PRIOR APPLICATION DATA:
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Patent No. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364 CATGCAAAAGAAACAGGCGCAAAATATTTTAACCTTGCTGGTCAAGCATACCAAAATCAA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
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FILING DATE: 30-Oct-1997
CLASSIFICATION: <UNKNOWN>
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APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
                                                            NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                   ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Maryland COUNTRY: USA
APPLICATION NUMBER:
FILING DATE:
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US-08-961-083-67
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APPLICANT: Matsuhisa, Akio
APPLICANT: Watsuhisa, Akio
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OP SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.5%; Score 38.4; DB 4; Length 3 Best Local Similarity 44.6%; Pred. No. 0.28; Matches 150; Conservative 0; Mismatches 186; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 AAAAACAATATCAGTAGTAAATCAACTACTAACAAT 343
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                                                                                   REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR EGG ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 base pairs
                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
SPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
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COUNTRY: United States of America
ZIP: 60606-6402
                          NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
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APPLICATION NUMBER: US/08/920,812
FILING DATE: 29-AUG-1997
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ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 IGTGAATCCGAATGAAACTGCATTATTAAATGAGTGGCGTGCTGATTTAGAAAATGGTAT 263
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4.5%; Score 38.4; DB 1; Length 10207;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 96; Conservative 0; Mismatches 96; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ohno, Tsuneya
APPLICANT: Ohno, Tsuneya
APPLICANT: Watsuhisa, Akio
APPLICANT: Ushara, Hirotsugu
APPLICANT: Ushara, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              i Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
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APPLICATION NUMBER: US/08/920,827 FILING DATE: 29-AUG-1997
PILING DATE: 29-AUG-1997
PILING DATE: 27-MAR-1995
FILING DATE: 27-MAR-1995
                                                                                                                                19036/32420
     US 08/362,577
                                                                                                                                                                                                                                                                                                                                                                                                                                 UKUANISM: Staphylococcus aureus ; STRAIN: Clinical Isolate SA-24 US-08-920-812-2
  APPLICATION NUMBER: US CO, 202,
FILING DATE: 27 MAR-1995
ATTORNEY/AGENT INPORMATION:
NAME: Rin-Leures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 33,547
REPERENCE/DOCKET NUMBER: 1903
TELERAX: 25.3856
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10207 base pairs
TYPE: nucleic acid
STRANDEDNES: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
CENTRAL SOURCE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
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Patent No. 5770375
GENERAL INFORMATION:
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APPLICATION NUMBER:
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**REGISTRATION NUMBER: 33.547

**REGISTRATION NUMBER: 312.440

**REGISTRATION NUMBER: 312.440

**REGISTRATION NUMBER: 312.440

**TELERA: 312.444-648

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Search completed: August 2, 2004, 04:12:30 Job time : 102 secs

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Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
E. Email: seqrefégenoscope.cns.fr. Web: www.genoscope.cns.fr
E. Inbirary was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6015.f
Contact: Peng Liang Email: fliang@lifetech.com URL:
Contact: Peng Liang Email: fliang@lifetech.com URL:
Chttp://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAP001DG01NP1.
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AL255309 Tetracdon
AL255309 Tetracdon
BH154104 EWTRB58TF
AL078714 DOSOPHII
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AL077728 Drosophil
AL46999 TY end of
AL536104 AL536104
AU034262 AU034262
AZ687764 ENTHD89TF
BM 64871 EST567394
BZ063272 Ikz69h12.
BJ376728 BJ376728
BX355654 BX355654
AZ677978 ENTHJ38TR
AL108704 Drosophil
AL206908 Tetracodon
AL226800 Tetracodon
BX61152 BX361152
BX462896 BX462896
BX462896 EKS702080
BZ69673 SP EEST02080
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AL106896 Drosophil
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BM162501 EST565024
AL063921 Drosophil
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Compugen Ltd.
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Scoring table:

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605 bp mRNA linear EST 04-DEC-2001
EST565024 PyBS Plasmodium yoelii yoelii cDNA clone PYCKT40 5' end,
mRNA sequence.
Cypriniformes; Cyprinidae; Danio.

(bases 1 to 844)

Humphray, S.J., Huckle, E. and Durham, J.L.

Humphray, S.J., Huckle, E. and Durham, J.L.

Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 iSA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished the Total of BAC 99E7. 99E7 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:

Reygene. Further details:

http://www.sanger.ac.uk/Projects/D_rerio/.
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1 (bases 1 to 605)
Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B., Praser, C.M. and Carucci, D.J.
Plasmodium yoelii EST project at TIGR
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47.2%; Pred. No. 0.029;
tive 0; Mismatches 177;
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Brasaite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD
9713 301-330-9319
Fax: 301-838-0208
Email: carlton@tigr.org
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                                                                                                                                                                                                                                                                /organism="Danto rerio"
/mol_type="genomic DNA"
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/clone="DKEY-9987"
/tissue_type="Testis"
/note="Vector pindigoBAC-536"
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                                                                                         /Lissue type="THYMUS"
/clone lib="Homo sapiens THYMUS"
/note="Wester: PCMVSPORT 6; lst strand cDNA was primed
/note="Wester: PCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and ECORV sites of the pCMVSPORT 6 vector.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCAT-TCTTCTACTTAGGATTATCGCTTCATTATTAGGAGATGTGAATCAGCCAATGC 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  554 TIGITGATACAATAAAAATAACTATATTGTTTCAGATAGCAATGGATATTGGAATTGGA 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 TACAACGATTGTGAATCCGAATGAAACTGCATTATTAAATGAGTGGCGTGCTGATTTAGA 254
                                                                                                                                                                                                                                                                                                                                                                           791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           494 AIGCAGCAAACTTTACGAATCTTTCTTATCCAATGGGTTTCCATTCTAAATACGAAATT 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Danio rerio (zebrafish)
Danio rerio
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostel; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAATGGTATTTATTCTGCTGATTACGAGAATCCTTATTATGATAATAGTACATATGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 AACAGGCGCAAAATATTTTAACCTTGCTGGTCAAGCATACCAAAATCAAGATATGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315 TCACTTTTATGATCCGGATACTGGAACATATATTCCTTTTGCGAAACATGCAAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   614 AAGGAGCAAACCCAGAAGATTGGATTGAAGGAGCAGCGGTAGCAGCTAAACAAGATTATC
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                1,
                                                                                                                                                                                                                                                                           DB 13; Length 994;
                                                                                                                                                                                                                                                                       Query Match

6.1%; Score 52.2; DB 13; Length
Best Local Similarity 20.7%; Pred. No. 0.024;
Matches 125; Conservative 202; Mismatches 276; Indels
                                                                                                                                                                                              the Not I and EcoRV sites of Library was not normalized.
                  organism="Homo sapiens"
                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOCAP001YN02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX139987.1 GI:27971314
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BX139987
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For clone info, please contact the Malaria Research and Reference

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Direct Submission

L Submitted (102-JUN-1999) Genoscope - Centre National de Sequencage:

Bp 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP brosophila melanogaster BAC library was prepared by Kazutcyo Geogeaw and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial ECORI digetion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                    CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             920 DDDGGGGGCDDGKGKDADDDTDGTKDDDDKDKWRDDWDKAKGTWGDATWAWAATDWWWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:|:::|::|| :: :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 TAACTCTCATTTGTGGATTGTAAATCGTGCAATTGACATCATGTCTCGTAATACAACGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 TGTGAATCCGAATGAAACTGCATTATTAAATGAGTGGCGTGCTGATTTAGAAAATGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323 ATGATCCGGATACTGGAACAACATATATTCCTTTTGCGAAACATGCAAAAGAAACAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 TTATTCTGCTGATTA-CGAGAATCCTTATTATGATAATAGTACATATGCTTCTCACTTTT
                                                                                                                                                                                                                                                                                                      Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                        Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.9%; Score 50.4; DB 29; Best Local Similarity 15.0%; Pred. No. 0.067; Matches 85; Conservative 254; Mismatches 226;
                                                                                                                                                                                                                                                                            (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/db_xref="texon:727"
/clone="macRo8x10"
/clone lib="RPCI 98"
/note="end : TET3"
                                                                                                                                                                    genomic survey sequence.
                                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                      AL063921.1 GI:4941778
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope
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                               RESULT 4
CNS0039G/c
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                                                                                                              DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven fermini were treated with Ptu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybrizAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-CAL4) was excised from the HybrizAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                       /dev stage="Nexual blood stages"
/lab_host="E. coli XL-1 Blue"
/clone_lib="PyBS"
/note="Vector: pAD-GAL4; At 20-25* parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was incloated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTACGAGAATCCTTATTATGATAATAGTACATATGCTTCTCACTTTTATGATCCGGATA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trggaattagicataacagaaraaarcctaarrcagcrcatgaaaaraaragigaaagic 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITCTTATCCAATGGGTTTCCATTCTAAATACGAAAATTTTGTTGATACAATAAAAATA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGAAATGGATGACGATGATGACGAAATTGAAGTTATCGATGAAATGATGAAGATG 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  516 AAATGGATGAAGATGATGATGATGATGATGATGACGATGAGATGAGGATGAGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGATGATATTCATTATGAATATGAAGAGGAAATGGACGATGATTATATAGATGAGGATG
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Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html
Seg primer: ADF.
                                                                                                                                  'organism="Plasmodium yoelii yoelii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.1%; Score 51.4; DB 12;
43.8%; Pred. No. 0.035;
tive 0; Mismatches 286;
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                                                                                                                                                                                                                                             db_xref="taxon:73239"
clone="PYCKT40"
                                                                                                                                                                                                                    sub_species="yoelii"
                                                                                  Location/Qualifiers
                                                                                                                                                              /mol_type="mRNA"
'strain="17XL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolated."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 43.8 Matches 223; Conservative
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375 AACAGGCGCAAAATATTTTAACCTTGCTGGTCAAGCATACCAAAATCAAGATATGCAGCA
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|lab_host="E. coli XL-1 Blue"
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/clone="PYCMD07"
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                                                                                                                                                                                                                                                                                                                                                                                    260 ATGTTGTTCTTATGGAAA 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
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Entamoeba histolytica
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.

1 (Dases 1 to 977)
1 (Dases 1 to 977)
2 Loftus; E., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI: IMSS sheared DNA library
Unpublished (2000)
Contact: Erchadan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@filgr.org
Clones are derived from the Entamoeba histolytica HMI: IMSS sheared
DNA library
Seq primer:
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                                                                                                                                                                                                                                                                                                                                977 bp DNA linear GSS 14-DEC-2000 ENTHDBUTF Entamoeba histolytica Sheared DNA Entamoeba histolytica AZ687764
                                                                                                                                                                 623 ACCCAGAAGATTGGATTGAAGGAGCAGCGGTAGCAGCTAAACAAGATTATCCTGGCGTTG 682
                                 ACTITIACGAATCITITCITATCCAATGGGITITCCATICTAAATACGAAAATTITGITGATA 562
                                                                                                                    620 KWDWKTRADRWDRWAADTWTDARKADRDWAKARAWRARRDRARADRRWTTKGKTTTA 561
800 RKRADDKRDAADDRDDAATWTTWTTTTRDTDDWKWKTDTWTRWAADRTWDRDDDDRDR 741
                                                               740 AGTAGRKWRRTWKRRWKRRDTRWDDADADDDTARDDRRRRGDDGADAGKGKKTGRKRRRD 681
                                                                                                  563 CAATAAAAATAACTATATTGTTTCAGATAGCAATGGATATTGGAATTGGAAAGGAGCAA
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49.4%; Pred. No. 0.084;
tive 0; Mismatches 160; Indels
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High quality sequence start: 58
High quality sequence stop: 493.
Location/Qualiflers
1.977
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Best Local Similarity 49.4<sup>1</sup>
Matches 157; Conservative
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source

ORIGIN

FEATURES

GSS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL COMMENT

RESULT 5 AZ687764/c DEFINITION

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BMI64871 634 bp mRNA linear EST 04-DEC-2001
EST567394 PyBS Plasmodium yoelii yoelii cDNA clone PYCMD07 5' end,
                                                       493
                                                                                                  441
                                                                                                                                               553
                                                                                                                                                                          613
                                                                                                                                                                                                                                                                                      321
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                                                                                                                                                                                                                                                                                                                                                                       320 ATGAAAGTAAAGAAGAAGAAGAAAGAAAGAACCTGAGTTTGAAGTTGATAATGATAATG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for clone info, please contact the Malaria Research and Reference
TTGTTGATACAATAAAAAAAAATAACTATATTGTTTCAGATAGCAATGGATATTGGAATTGGA
                                                         135 AGCATTCTTCTACTTAGGATTATCGCTTCATTA-TTTAGGAGATGTGAATCAGCCAATGC
                                                                                                    500 TIGAAGAAGTIATIAAATAIGCAAAATICAITAGIGGAACGGIIGCACAACAACCIT
                                                                                                                                               494 ATGCAGCAAACTTTACGAATCTTTATCCAATGGGTTTCCATTCTAAATACGAAAATT
                                                                                                                                                                                                                                                                                   380 GIGITGAITTATIAGAAAAIGCTGGATGGAAIAGAGAIATTACIGCGIACAGIGAITCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carlton,J.M., Dally,T.M., Long,C.A., Bergman,L.W., Valdya,A.B., Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
I (bases 1 to 634)
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The static Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
1911-301-530-9319
Fax: 301-838-0208
Email: carlton@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html

    634
/organism="Plasmodium yoelii yoelii"
/mol_type="mRNA"
/strain="17XL"
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Gaps

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691 387 EST 08-MAR-2002

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313 TCTCACTTTTATGATCCGGATACTGGAACAACATATATTCCTTTTGCGAAACATGCAAAA 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BJ376728 Bictyostelium discoideum cDNA linear EST 08-MAR-20
BJ376728 Dictyostelium discoideum cDNA library, CF Dictyostelium
discoideum cDNA clone ddc29013 3', mRNA sequence.
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Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (Dases I to 754)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the culmination
                                                                                                                                   750 TCTTATTATGCGAGAACAGTATTTTCTTATTATCAAAGTTGTATCTTATATTTATAN
                                                                                                                                                                                328 CCGGATACTGGAACAACATATATTCCTTTTGCGAAACATGCAAAAGAAACAGGCGCAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 AATACAACGATIGIGAATCCGAATGAAACTGCATTATTAAATGAGTGGCGTGCTGATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="Culmination stage"
/clone_lib="Dictyostelium discoideum cDNA library,
  Length 776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12; Length 754;
                                               Indels
                                                                                         TCTGCTGATTACGAGAATCCTTATTATGATAATAGTACATATGCTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2002)
Contact: Tadasu Shin-i
Contex For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Far: 81-559-81-6855
    DB 28;
  Score 48.2; DB 28;
Pred. No. 0.23;
0; Mismatches 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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BJ376728.1 GI:19286111
5.7%;
llarity 50.7%;
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                            Best Local Sim
Matches 113;
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                                                                                           268
       Query Match
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TITLE
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termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybrizApP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosida; eurosida II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 776)

Delehaunty.K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,

Nash,W., Rabinowicz,P.D. and Wilson,R.K.

Whole genome shotgun reads from Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="Bolleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHI) and the Sequencing Center.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      726
                                                                                                                                                                                                                                                                                                                    547 GAAAATTTTGTTGATACAATAAAAATAACTATATTGTTTCAGATAGCAATGGATATTGG 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATTGGAAAGGAGCAAAACCCAGAAGATTGGATTGAAGGAGCAGCGGTAGCAGCTAAACAA
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                                                                                                                                                                                                                        Score 49.2; DB 12; Length 634;
Pred. No. 0.12;
0; Mismatches 113; Indels 0
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Genome Sequencing Center
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: 1kz69 row: h column: 12
Seq primer: -21UFpOT forward
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/db xref="taxon:3712"
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High quality sequence stop: 551.
Location/Qualifiers
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                                                                                                                                                           isolated."
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Matches 117; Conservative
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525 CCAGAAGATTGGAATGGAGGAGCAGCGGTAGCAGCTAAACAAGATTATCCTGGCGTTGTG 684
                                                                                                                                                                                                                                                                                                            GKADGAAAKGGAAAAAAAAAAAAAAAAABKKKAAAAADAAKKAKGARKKKRAKGAAA
                                                                                                                                                            685 AACGATACGACAAAAGATTGGTTTGTAAAAGCAGCCGTATCTCAAGAATATGCAGATAAA
                                                                                                                                                                                                                                                                         745 TGGCGTGCGGAAGTAACACCGGTGACAGGAAAGCGTTTAATGGAAAGCGCAGCGCTTACA
                                                                                                                                                                                                                                                                                                                                                                                      805 GCTGGTTATATTCATTTGTGGTTTGATACGTATGTAAA 842
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Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 862)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the 
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/strain="HM1:IMSS"
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High quality sequence start: 15
High quality sequence stop: 862.
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Contact: Genoscope.
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - Prance
BRaall: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI002BC06NP1.
CAAGCATTCTTCTACTTAGGATTATCGCTTCATTATTTAGGAGATGTGAATCAGCCAATG 492
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Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
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//mol_type="mRNA"
//db_xref="texon:0566"
//db_xref="texon:0566"
/clone="CSOIO02YE12"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone="Ish = Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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llarity 28.6%; Pred. No. 0.31;
Conservative 110; Mismatches 214; Indels 3;
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Li,W B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/db_xrefe="traxon:5759"
/db_xrefe="traxon:5759"
/clone lib="Entamoeba histolytica Sheared DNA"
/note=="Vector: pHOS1; Site=:1 BBt 1; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, L.S. (1991) Entamoeba histolytica: method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter' J.C. (Making small insert libraries for when the construction is described in detail in Smith, the library construction is described in detail in Smith, the library construction is described in detail in Smith, the library construction is described in detail in Smith, the library construction is described in detail in Smith, the library construction is described in detail in Smith, the library construction is described in detail in Smith, the library construction is described in detail in Smith, the library construction is described in detail in Smith, the library construction is described in detail in Smith, the library construction is described in detail in Smith, the library construction is described in detail in Smith, the library construction is described in detail in Smith, the library construction is described in detail in Smith, the library construction is described in detail the library construction is described in detail the library construction is described in detail the library construction is described in detail the library construction is described in detail the library construction is described in detail the library construction is described in detail the library construction is described in detail the library construction is described in detail the library construction is described in detail the library construction is described in detail the library construction is described in detail the library construction is describe
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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
Seq primer: M13-Reverse
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Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Fax: 301 838 9298
940 ARADKKGAKAWITWAWITATTTTTAAATDWATKAAWA 977
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Direct Submitssion
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 BVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
904 ATATTATWATAWTWATATATWTWWWWTWAAAWAATTWWWWWTATWTATATATATAW
                                                                       ATATATTCCTTTTGCGAAACATGCAAAAGAAACAGGCGCAAAATATTTTAACCTTGCTGG
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Characterization and repeat analysis of the compact genome of greshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
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"mol type="genomic DNA"
|db_xref="taxon:99883"
|clone="153P04"
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GSS; genome survey sequence.
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Tetraodon nigroviridis
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etded un Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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  AGGCGCAAAATATTTTAACCTTGCTGGTCAAGCATACCAAAATCAAGATATGCAGCAAGC 437
                                            26 AAGTGCAAAAGATTGTTGCATGAATGAAAGGGTTAAACAAAATAACGTTTATACCATTG
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Larity 29.6%; Pred. No. 0.48;
Conservative 81; Mismatches 185; Indels
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|mol_type="genomic DNA"
|db_xref="taxon:7227"
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AL22680.1 GI:7885817
GSS; genome survey sequence.
Tetracdon nigroviridis
Tetracdon nigroviridis
Bukaryota, Metaca, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetracdontiformes,
Tetradontoidea, Tetracdontidae; Tetracodon.
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                                                                                                                                                                                                               315 TCACTITIAIGAICCGGAIACTGGAACAACAIAIATITCCTITITGCGAAACAIGCAAAAGA 374
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Estinate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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/clone_lib="G"
/note="Genoscope sequence_ID : COAG153DH02SP1~end
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Best Local Similarity 36.6%; Pred. No. 0.54;
Matches 132; Conservative 37; Mismatches 192; Indels
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Contact: Genoscope
Genoscope - Centra National de Sequencage
Genoscope - Centra National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Inbitary was constructed by life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7593.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=cc001081AB10QP1&cluster=7593.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
Peng Liang Email: fliang@lifetech.com URL:
Peng Liang Avenue Genoscope sequence ID: CS0D1081AB10QP1.
Location/Qualifiers
                                                                                             Web: www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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1 (hases I to 1201)
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Full.length CDNA libraries and normalization
Unpublished (2001)
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/mol type="genomic DNA"
/mol type="genomic DNA"
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/clone="211K19"
/clone lib="G"
/note="Genoscope sequence ID : COAG211AF10SF1~end
/proce="Genoscope sequence ID : COAG211AF10SF1~end
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Best Local Similarity 41.0%; Pred. No. 0.64;
Matches 105; Conservative 29; Mismatches 122;
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/organism="Homo sapiens"
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Search completed: August 2, 2004, 04:10:48 Job time : 2820 Reca
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BX462896 Homo sapiens FETAL LIVER Homo sapiens cDNA clone CSODM001XL14 3-PRIME, mRNA sequence.
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                               /clone="CSODIO81Y019"
/tissue type="PLACENTA COT 25-NORMALIZED"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NOTI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4458.r F http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSODMO01DFO7NPl&cluster=4458.r. Contac Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODMO01DF07NPl.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1201)

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36.7%; Pred. No. 0.87;
iive 37; Mismatches 182; Indels
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
FN11-length cDNA libraries and normalization
Unpublished (2001)
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - Prance
/mol_type="mRNA"
/db_xref="taxon:9606"
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Matches 127; Conservative
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/tissue type="FETAL LIVER"
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/dev_stage="fetal"
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/note="Organ: liver; Vector: pCMVSFORT_6; 1st strand cDNA was primed with a NotI-oligo (df) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORY sites of the pCMVSFORT 6 vector. Library was not normalized."
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Matches 148; Conservative
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